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(71) Applicant *(for all designated States except US)*: ASTRA AKTIEBOLAG [SE/SE]; S-151 85 Södertälje (SE).

(72) Inventor; and
(75) Inventor/Applicant *(for US only)*: SMITH, Douglas, H. [US/US]; 2 Mayflower Lane, Gloucester, MA 01930 (US).

(74) Agents: HANLEY, Elizabeth, A. et al.; Lahive & Cockfield, 60 State Street, Boston, MA 02109 (US).

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(54) Title: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS

(57) Abstract

Recombinant or substantially pure preparations of *H. pylori* polypeptides are described. The nucleic acids encoding the polypeptides also are described. The *H. pylori* polypeptides are useful in vaccine compositions.

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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *HELICOBACTER PYLORI* FOR DIAGNOSTICS AND THERAPEUTICS

Background of the Invention

Helicobacter pylori is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is accumulating for an etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human gastric mucosa, establishing an infection that usually persists for decades. Infection by *H. pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of the putative virulence factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6: 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci.* USA 90: 2035-203).

Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo* because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availabilty. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics combined with bismuth are part of the standard regime used to treat *H. pylori* infection. (Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the problem of the

emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, supra). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

Summary of the Invention

This invention relates to novel genes, e.g., genes encoding bacterial surface proteins, from the organism *Helicobacter pylori*, and other related genes, their products, and uses thereof. The nucleic acids and peptides of the present invention have utility for diagnostic and therapeutics for *H. pylori* and other *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* surface proteins or parts thereof, nucleic acids capable of binding mRNA from *H. pylori* surface proteins to block protein translation, and methods for producing *H. pylori* surface proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also includes antibodies and nucleic acids sequences useful as probes to detect *H. pylori* infection. In addition, vaccine compositions and methods for the protection against infection by *H. pylori* are described.

Brief Description of the Drawings

Figure 1 is a table which contains information from homology searches performed on the sequences of this invention using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package.

Figure 2 is a bar graph that depicts the antibody titer in serum of mice following immunization with specific *H. pylori* antigens.

Figure 3 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 5 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in buffer containing DOC.

Detailed Description of the Invention

In one aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:115, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:1.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:116, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:2.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:117, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:3.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:118, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:4.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:119, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:5.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:120, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:6.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:121, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:7.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:122, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:8.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:123, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:9.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:124, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:10.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:125, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:11.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:126, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:12.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:127, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:13.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:128, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:14.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:129, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:15.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:130, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:16.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:131, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:17.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:132, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:18.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:133, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:19.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:134, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:20.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:135, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:21.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:136, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:22.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:137, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:23.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:138, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:24.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:139, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:25.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:140, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:26.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:141, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:27.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:142, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:28.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:143, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:29.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:144, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:30.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:145, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:31.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:146, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:32.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:147, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:33.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:148, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:34.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:149, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:35.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:150, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:36.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:151, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:37.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:152, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:38.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:153, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:39.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:154, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:40.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:155, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:41.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:156, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:42.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:157, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:43.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:158, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:44.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:159, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:45.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:160, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:46.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:161, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:47.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:162, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:48.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:163, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:49.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:164, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:50.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:165, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:51.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:166, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:52.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:167, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:53.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:168, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:54.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:169, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:55.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:170, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:56.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:171, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:57.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:172, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:58.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:173, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:59.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:174, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:60.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:175, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:61.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:176, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:62.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:177, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:63.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:178, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:64.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:179, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:65.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:180, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:66.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:181, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:67.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:182, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:68.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:183, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:69.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:184, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:70.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:185, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:71.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:186, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:72.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:187, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:73.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:188, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:74.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:189, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:75.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:190, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:76.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:191, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:77.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:192, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:78.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:193, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:79.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:194, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:80.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:195, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:81.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:196, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:82.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:197, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:83.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:198, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:84.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:199, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:85.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:200, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:86.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:201, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:87.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:202, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:88.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:203, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:89.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:204, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:90.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:205, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:91.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:206, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:92.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:207, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:93.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:208, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:94.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:209, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:95.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:210, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:96.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:211, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:97.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:212, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:98.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:213, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:99.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:214, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:100.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:215, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:101.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:216, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:102.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:217, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:103.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:218, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:104.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:219, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:105.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:220, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:106.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:221, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:107.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:222, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:108.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:223, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:109.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:224, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:110.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:225, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:111.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:226, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:112.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:227, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:113.

In another aspect, the invention features a substantially pure nucleic acid encoding an *H. pylori* polypeptide having an amino acid sequence of SEQ ID NO:228, such as a nucleic acid comprising a nucleotide sequence of SEQ ID NO:114.

In another aspect, the invention comprises nucleic acids capable of binding mRNA of *H. pylori*. Such nucleic acid is capable of acting as anti-sense nucleic acid to control the translation of mRNA of *H. pylori*. A further aspect features a nucleic acid which is capable of binding specifically to an *H. pylori* nucleic acid. Such nucleic acid has utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *H. pylori* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *H. pylori* nucleic acid.

In another aspect, the invention features a cell transformed with the expression system to make *H. pylori* polypeptides.

In another aspect, the invention features a method of generating antibodies against *H. pylori* proteins which are capable of binding specifically to *H. pylori* proteins. Such antibody has utility as reagents for immunoassays to evaluate the abundance and distribution of *H. pylori*-specific antigens.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *H. pylori*. The method includes: immunizing a subject with an *H. pylori* protein, e.g., a surface protein, or portion thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention provides a method for generating a vaccine comprising a modified immunogenic *H. pylori* protein, e.g., a surface protein, or portion thereof, and a pharmacologically acceptable carrier.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* polypeptide. The method includes: contacting the candidate compound with an *H. pylori* polypeptides and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate compound with an *H. pylori* nucleic acid and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

The invention features, *H. pylori* polypeptides, preferably a substantially pure preparation of an *H. pylori* polypeptide, or a recombinant *H. pylori* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence contained in SEQ ID NOs:115-228; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence in SEQ ID NOs:115-228; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the polypeptide includes at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acids contained in SEQ ID NOs:115-228.

In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid in SEQ ID NOs:1-114, or by a nucleic acid having at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of SEQ ID NOs:1-114.

In a preferred embodiment, the subject *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues from a sequence in SEQ ID NOs:115-228. The differences, however, are such that: the *H. pylori* polypeptide exhibits an *H. pylori* biological activity, e.g., the *H. pylori* polypeptide retains a biological activity of a naturally occurring *H. pylori* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence contained in SEQ ID NOs:115-228; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' to the genomic DNA which encodes a sequence contained in SEQ ID NOs:115-228.

In yet other preferred embodiments, the *H. pylori* polypeptide is a recombinant fusion protein having a first *H. pylori* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *H. pylori*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a

DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

The invention includes an immunogen which includes an *H. pylori* polypeptide in an immunogenic preparation, the immunogen being capable of eliciting an immune response specific for said *H. pylori* polypeptide, e.g., a humoral response, an antibody response, or a cellular response. In preferred embodiments, the immunogen comprises an antigenic determinant from a protein contained in SEQ ID NOs:115-228.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *H. pylori* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity the encoded polypeptide has an amino acid sequence at least 60%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence contained in SEQ ID NOs:115-228; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence in SEQ ID NOs:115-228; the encoded polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acids contained in SEQ ID NOs:115-228.

In preferred embodiments: the nucleic acid is that of SEQ ID NOs:1-114; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence contained in SEQ ID NOs:1-114.

In a preferred embodiment, the encoded *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence in SEQ ID NOs:115-228. The differences, however, are such that: the *H. pylori* encoded polypeptide exhibits a *H. pylori* biological activity, e.g., the encoded *H. pylori* enzyme retains a biological activity of a naturally occurring *H. pylori*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence contained in SEQ ID NOs:115-228; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' to the genomic DNA which encodes a sequence contained in SEQ ID NOs:115-228.

In preferred embodiments, the subject *H. pylori* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *H. pylori* gene sequence, e.g., to render the *H. pylori* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *H. pylori* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe

corresponding to at least 12 consecutive nucleotides contained in SEQ ID NOs:1-114; more preferably to at least 20 consecutive nucleotides contained in SEQ ID NOs:1-114; more preferably to at least 40 consecutive nucleotides contained in SEQ ID NOs:1-114.

In a preferred embodiment, the nucleic acid encodes a peptide which differs by at least one amino acid residue from the sequences shown in SEQ ID NOs:115-228.

In a preferred embodiment, the nucleic acid differs by at least one nucleotide from a nucleotide sequence shown in SEQ ID NOs:1-114 which encodes amino acids shown in SEQ ID NOs:115-228.

In another aspect, the invention includes: a vector including a nucleic acid which encodes an *H. pylori*-like polypeptide, e.g., an *H. pylori* polypeptide; a host cell transfected with the vector; and a method of producing a recombinant *H. pylori*-like polypeptide, e.g., an *H. pylori* polypeptide; including culturing the cell, e.g., in a cell culture medium, and isolating the *H. pylori*-like polypeptide, e.g., an *H. pylori* polypeptide, e.g., from the cell or from the cell culture medium.

In another aspect, the invention features, a purified recombinant nucleic acid having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence contained in SEQ ID NOs:1-114.

The invention also provides a probe or primer which includes a substantially purified oligonucleotide. The oligonucleotide includes a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence contained in SEQ ID NOs:1-114, or naturally occurring mutants thereof. In preferred embodiments, the probe or primer further includes a label group attached thereto. The label group can be, e.g., a radioisotope, a fluorescent compound, an enzyme, and/or an enzyme co-factor. Preferably the oligonucleotide is at least 10 and less than 20, 30, 50, 100, or 150 nucleotides in length.

The invention involves nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

The *H. pylori* strain, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection(ATCC # 55679) as strain HP-J99.

The nucleic acid sequences of this invention may be obtained directly from the DNA of the above referenced *H. pylori* strain by using the polymerase chain reaction (PCR). See "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in this invention may be obtained by screening the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or

plaques as known in the art (see, eg, Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences.

As probes, primers, capture ligands and antisense agents, the nucleic acid will normally comprise approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products.

Putative functions have been determined for several of the *H. pylori* polypeptides of the invention, as shown in Figure 1.

Accordingly, uses of the claimed *H. pylori* polypeptides in these identified functions are also within the scope of the invention.

In addition, the present invention encompasses *H. pylori* polypeptides characterized as shown in Table 1 below, including: *H. pylori* outer membrane proteins, *H. pylori* periplasmic/secreted proteins, and other *H. pylori* surface proteins. Members of these groups were identified by BLAST homology searches. The *H. pylori* polypeptides identified in Table 1 are representative members of the groups identified above and are in no way limiting. Additional members of the groups can be identified within the *H. pylori* polypeptides disclosed herein by the methods known to those skilled in the art.

TABLE 1

SEQ ID NO	Blast identifier	Gene Symbol/Name	Description
Outer Membrane Proteins			
7116626 (SEQ ID NO:223)	P26093	e (P4)	e (P4) lipoprotein attached by lipid in *H. influenza*
29479681 (SEQ ID NO:179)	P13036	fecA	Receptor in Iron (III) dicitrate transport *E. coli*
36126938 (SEQ ID NO:199)	L12346	copB	Major out. memb. prot. in *M. catarrhalis*
Periplasmic/Secreted Proteins			
30100332 (SEQ ID NO:181)	P23847	dppA	Periplasmic dipeptide binding protein in *E. coli*
Other Surface Proteins			
4821082 (SEQ ID NO:212)	P08089	M protein	M protein of group *A. Streptococci*
978477 (SEQ ID NO:228)	L28919	FBP54	Surface Ag of grp *A. Streptococci* binds fibronectin

Definitions

A purified preparation or a substantially pure preparation of a polypeptide, as used herein, means a polypeptide that has been separated from other proteins, lipids. and nucleic

acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to allow protein sequencing; at least 1, 10, or 100 µg of the polypeptide; at least 1, 10, or 100 mg of the polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an in vitro preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

The metabolism of a substance, as used herein, means any aspect of the, expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A substantially pure nucleic acid, e.g., a substantially pure DNA, is a nucleic acid which is one or both of: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid sequence with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *H. pylori* DNA sequence.

Homologous refers to the sequence similarity or sequence identity between two polypeptide molecules or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10, of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50%

homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

As used herein, the term "transgene" means a nucleic acid sequence (encoding, e.g., one or more polypeptides), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the cell's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of the selected nucleic acid, all operably linked to the selected nucleic acid, and may include an enhancer sequence.

As used herein, the term "transgenic cell" refers to a cell containing a transgene.

As used herein, a "transgenic animal" is any animal in which one or more, and preferably essentially all, of the cells of the animal includes a transgene. The transgene can be introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

A polypeptide has *H. pylori* biological activity if it has one, two, three, and preferably more of the following properties: (1) if when expressed in the course of an *H. pylori* infection, it can promote, or mediate the attachment of *H. pylori* to a cell (2) it has an enzymatic activity characteristic of an *H. pylori* protein (3) or the gene which encodes it can rescue a lethal mutation in an *H. pylori* gene. A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of

expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-transitional modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site and terminators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a peptide. This region may represent a portion of a coding sequence or a total sequence.

As used herein, a "coding sequence" is a nucleic acid sequence which is transcribed into messenger RNA and/or translated into a peptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three

prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, or recombinant nucleic acid sequences.

A "gene product" is a protein or structural RNA which is specifically encoded for by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

The experimental manipulation of such conditions has been well described in the literature including such books as *Molecular Cloning; A Laboratory Manual*, Sambrook, J., Fritsch, E.F., Maniatis, T., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 2nd ed. (1989).

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See e.g.*, Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.) and *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991).

Probes

A nucleic acid isolated or synthesized in accordance with SEQ ID NOs:1-114 can be used as a probe to specifically detect *H. pylori.* With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *H. pylori*, and extraneous nucleic acid sequences likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least twenty to thirty nucleotides to convey

stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acid sequences, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with SEQ ID NOs:1-114 may also be useful as probes to detect homologous regions (especially homologous genes) of other *Helicobacter* species using relaxed stringency hybridization conditions, as will be obvious to anybody skilled in the art.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence contained in SEQ ID NOs:1-114 have utility to separate *H. pylori* nucleic acid from the nucleic acid of each other and other organisms. Nucleic acid having twenty or more nucleotides in a sequence shown in SEQ ID NOs:1-114 may also have utility to separate other *Helicobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least twenty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility as primers for the amplification of *H. pylori* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acid sequences in other *Helicobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of $\geq$ 10-15 nucleotides contained in SEQ ID NOs:1-114 have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori* nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *H. pylori* and/or other *Helicobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as will be described in greater detail below.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *H. pylori* genes. These sequences may also have utility as antisense agents to prevent expression of genes of other *Helicobacter* species.

Nucleic acid or derivatives corresponding to *H. pylori* nucleic acid sequences is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

Expressing *H. pylori* Genes

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression could be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to other *Helicobacter* strains, and other bacterial strains such as *E. coli*, *Norcardia*, *Corynebacterium*, and *Streptomyces* species. In some cases the expression host will utilize the natural *Helicobacter* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *H. pylori* promoter, a procedure such as the following is used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing the following

components: an origin of replication that functions in the host organism, and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

Expressed Genes in Therapeutics

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate proteins and peptides. The nucleic acid exemplified in SEQ ID NOs:1-114 or fragments of said nucleic acid sequences encoding immunogenic portions of *H. pylori* proteins (SEQ ID NO:115-228) can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The host cell may be any procaryotic or eucaryotic cell. For example, an *H. pylori* peptide may be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cell (CHO). Other suitable host cells are known to those skilled in the art.

Expression in eucaryotic cells such as mammalian, yeast, or insect cells can lead to partial or complete glycosylation and/or formation of relevant inter- or intra-chain disulfide bonds of a recombinant peptide product. Examples of vectors for expression in yeast *S. cerivisae* include pYepSec1 (Baldari. et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Baculovirus vectors available for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39). Generally, COS cells (Gluzman, Y., (1981) *Cell* 23:175-182) are used in conjunction with such vectors as pCDM 8 (Aruffo, A. and Seed, B., (1987) *Proc. Natl. Acad. Sci. USA* 84:8573-8577) for transient amplification/expression in mammalian cells, while CHO (dhfr$^-$ Chinese Hamster Ovary)

cells are used with vectors such as pMT2PC (Kaufman et al. (1987), *EMBO J.* 6:187-195) for stable amplification/expression in mammalian cells. Vector DNA can be introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, or electroporation. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

Expression in procaryotes is most often carried out in *E. coli* with either fusion or non-fusion inducible expression vectors. Fusion vectors usually add a number of NH_2 terminal amino acids to the expressed target gene. These NH_2 terminal amino acids often are referred to as a reporter group. Such reporter groups usually serve two purposes: 1) to increase the solubility of the target recombinant protein; and 2) to aid in the purification of the target recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the reporter group and the target recombinant protein to enable separation of the target recombinant protein from the reporter group subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase, maltose E binding protein, or protein A, respectively, to the target recombinant protein. A preferred reporter group is poly(His), which may be fused to the amino or carboxy terminus of the protein and which renders the recombinant fusion protein easily purifiable by metal chelate chromatography.

Inducible non-fusion expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). While target gene expression relies on host RNA polymerase transcription from the hybrid trp-lac fusion promoter in pTrc, expression of target genes inserted into pET11d relies on transcription from the T7 gn10-lac 0 fusion promoter mediated by coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 under the transcriptional control of the lacUV 5 promoter.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *H. pylori* peptide can be cultured under appropriate conditions to allow expression of the peptide to occur. The peptide may be secreted and isolated from a mixture of cells and medium containing the peptide. Alternatively, the peptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for

cell culture are well known in the art. Peptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptides. Additionally, in many situations, peptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Several different criteria are used for choosing a detergent suitable for solubilizing these complex. For example, one property considered is the ability of the detergent to solubilize the *H. pylori* protein within the membrane fraction at minimal denaturation of the membrane-associated protein allowing for the activity or functionality of the membrane-associated protein to return upon reconstitution of the protein. Another property considered when selecting the detergent is the critical micells concentration (CMC) of the detergent in that the detergent of choice preferably has a high CMC value allowing for ease of removal after reconstitution. A third property considered when selecting a detergent is the hydrophobicity of the detergent. Typically, membrane-associated proteins are very hydrophobic and therefore detergents which are also hydrophobic, e.g. the triton series, would be useful for solubilizing the hydrophobic proteins. Another property important to a detergent can be the capability of the detergent to remove the *H. pylori* protein with minimal protein-protein interaction facilitating further purification. A fifth property of the detergent which should be considered is the charge of the detergent. For example, if it is desired to use ion exchange resins in the purification process then preferably detergent should be an uncharged detergent. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *H. pylori* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding *H. pylori* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids*

Res. 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Drug Screening Assays

By making available purified and recombinant *H. pylori* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *H. pylori* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *H. pylori* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the skilled artisan.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *H. pylori* polypeptide.

Screening assays may be constructed *in vitro* with a purified *H. pylori* enzyme such that the action of the enzyme produces an easily detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds may be tested in the assay to identify those which inhibit or potentiate the activity of the *H. pylori* enzyme. Some of these active compounds may directly, or with

chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same enzymatic activity in whole, live *H. pylori* cells.

Antibodies

The invention also includes antibodies specifically reactive with the subject *H. pylori*-like polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *H. pylori* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *H. pylori* polypeptides of the invention, e.g. antigenic determinants of a polypeptide shown in SEQ ID NOs:115-228 or a closely related human or non-human mammalian homolog (e.g. 90% percent homologous, more preferably at least 95 percent homologous). In yet a further preferred embodiment of the present invention, the anti-*H. pylori* antibodies do not substantially cross react (i.e. react specifically) with a protein which is: e.g., less than 80% percent homologous to a sequence shown in SEQ ID NOs:115-228. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein contained in SEQ ID NOs:115-228. In a most preferred embodiment, there is no crossreactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *H. pylori* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, $F(ab')_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules having an anti-*H. pylori* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *H. pylori* polypeptides or *H. pylori* polypeptide variants, and antibody fragments such as Fab` and $F(ab`)_2$, can be used to block the action of *H. pylori* polypeptide and allow the study of the role of a particular *H. pylori* polypeptide of the present invention in aberrant or unwanted

intracellular signaling, as well as the normal cellular function of the *H. pylori* and by microinjection of anti-*H. pylori* polypeptide antibodies of the present invention.

Antibodies which specifically bind *H. pylori* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *H. pylori* antigens. Anti-*H. pylori* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *H. pylori* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *H. pylori* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *H. pylori* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*H. pylori* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *H. pylori* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *H. pylori* antigens.

Another application of anti-*H. pylori* polypeptide antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of ß-galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *H. pylori* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*H. pylori* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *H. pylori* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

Vaccines

The present invention also includes vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection, a gram-negative spiral microaerophilic bacterium. In one embodiment, the vaccine compositions contain immunogenic surface proteins from *H. pylori*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids shown in SEQ ID NOs:1-114 and which encode *H. pylori* surface proteins shown in SEQ ID NOs:115-228. However, any nucleic acid encoding an immunogenic *H. pylori* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines can have therapeutic and prophylactic utilities.

Another aspect of the present invention provides vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection. which contain a modified immunogenic *H. pylori* protein or portion thereof, and a pharmaceutically acceptable carrier. It is possible to modify the structure of a *H. pylori* protein or peptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *H. pylori* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition.

Another example of modification of an *H. pylori* peptide is substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *H. pylori* protein or peptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *H.pylori* protein can be modified using polyethylene glycol (PEG) according to the method of A. Sehon and co-workers (Wie et al., supra) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *H. pylori* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, supra); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *H. pylori* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of T cell epitopes within an *H. pylori* protein of the invention, canonical protease sensitive sites can be engineered between regions, each comprising at least one T cell epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The

resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more T cell epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Site-directed mutagenesis of a nucleic acid encoding an *H. pylori* protein can be used to modify the structure of the peptide by methods known in the art. Such methods may, among others, include polymerase chain reaction (PCR) with oligonucleotide primers bearing one or more mutations (Ho et al., (1989) *Gene*, 77: 51 - 59) or total synthesis of mutated genes (Hostomsky, Z. et al., (1989) *Biochem. Biophys. Res. Comm*, 161: 1056 - 1063). To enhance recombinant protein expression, the aforementioned methods can be applied to change the codons present in the cDNA sequence of the invention to those preferentially utilized by the host cell in which the recombinant protein is being expressed (Wada et al., supra). An extensive discussion of mutagenesis protocols is provided in the "Production of Fragments and Analogs" section herein.

Another aspect of the invention provides a vaccine composition for protection against infection by *H. pylori* which contains an immunogenic fragment of an *H. pylori* protein or portion thereof, and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic peptides of the invention can be obtained, for example, by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *H. pylori* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, an *H. pylori* protein may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptides having the ability to induce a T cell response, such as stimulation (proliferation, cytokine secretion). An extensive discussion of peptide analogs and fragments is provided in the "Production of Fragments and Analogs" section herein.

In one embodiment, immunogenic *H. pylori* fragments can be identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of

an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. One isotype of these antibodies, IgE, is fundamentally important to the development of allergic symptoms and its production is influenced early in the cascade of events at the level of the T helper cell, by the nature of the lymphokines secreted. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition. Amino acid sequences which mimic those of the T cell epitopes and which modify the allergic response to protein allergens are within the scope of this invention.

In another embodiment, immunogenic components of the invention are identified through genomic vaccination. The basic protocol is based on the idea that expression libraries consisting of all or parts of a pathogen genome, e.g., an *H. pylori* genome, can confer protection when used to genetically immunize a host. This expression library immunization (ELI) is analogous to expression cloning and involves reducing a genomic expression library of a pathogen, e.g., *H. pylori*, into plasmids that can act as genetic vaccines. The plasmids can also be designed to encode genetic adjuvants which can dramatically stimulate the humoral response. These genetic adjuvants can be introduced at remote sites and act as well extracelluraly as intracellularly.

This is a new approach to vaccine production that has many of the advantages of live/attenuated pathogens but no risk of infection. An expression library of pathogen DNA is used to immunize a host thereby producing the effects of antigen presentation of a live vaccine without the risk. For example, in the present invention, random fragments from the *H. pylori* genome or from cosmid or plasmid clones, as well as PCR products from genes identified by genomic sequencing, can be used to immunize a host. The feasibility of this approach has been demonstrated with *Mycoplasma pulmonis* (Barry et al., *Nature* 377:632-635, 1995), where even partial expression libraries of *Mycoplasma pulmonis*, a natural pathogen in rodents, provided protection against challenge from the pathogen.

ELI is a technique that allows for production of a non-infectious multipartite vaccine, even when little is known about pathogen's biology, because ELI uses the immune system to screen candidate genes. Once isolated, these genes can be used as genetic vaccines or for development of recombinant protein vaccines. Thus, ELI allows for production of vaccines in a systematic, largely mechanized fashion.

Screening peptides for those which are immunogenic can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture.

Presentation of an immunogenic *H. pylori* peptide in association with appropriate MHC molecules, to T cells, in conjunction with the necessary costimulation, has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ^{3}H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

To produce modified proteins or immunogenic fragments by recombinant DNA techniques, an expression vector containing a nucleic acid encoding all or a portion of a *H. pylori* protein, operably linked to at least one regulatory sequence can be used. Operably linked is intended to mean that the nucleotide sequence is linked to a regulatory sequence in a manner which allows expression of the nucleotide sequence. Regulatory sequences are art-recognized and include promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transformed and/or the type of protein desired to be expressed. In one embodiment of the present invention, the expression vector includes nucleic acid, preferably a DNA, encoding a modified *H. pylori* protein or immunogenic fragment having all or a portion of the amino acid sequence . Such expression vectors can be used to transfect cells to thereby produce proteins or peptides, including fusion proteins or peptides encoded by nucleic acids as described herein.

Host cells suitable for transfection and recombinant production of *H. pylori* proteins of the invention include any procaryotic or eucaryotic cell. For example, an *H. pylori* protein or peptide may be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cells (CHO). Other suitable host cells can be found in Goeddel, (1990) *supra* or known to those skilled in the art.

H. pylori proteins and fragments of the invention can also be chemically synthesized, using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. The nucleic acids of the invention can also be chemically

synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (see e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al., U.S. Patent No. 4,458,066; and Itakura, U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Vaccine compositions of the present invention containing DNA encoding immunogenic protein from *H. pylori*, or containing modified protein or fragments, contain both the DNA or protein and a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing modified *H. pylori* protein or immunogenic protein fragments, the protein or peptide must be coadministered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *H. pylori*. Czinn et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphos-phoryloxy)-ethylamine (CGP 19835A, referred to a MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycoloate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80

emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholeragenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*H. pylori* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immuno-stimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 μg to 50 μg, for example 10 μg to 35 μg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *H. pylori* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO3 and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *H. pylori* in an infected host, or as a therapeutic agent with the aim to induce an immune response in a susceptible host to prevent infection by *H. pylori*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 μg to 10 g, preferably 10 μg to 100 mg, for example 50 μg to 50 mg. A suitable dosage for adults will also be in the range of 5 μg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less dependant upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses

for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *H. pylori* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *H. pylori* infection, some are useful only for treating *H. pylori* infection, and some are useful for both preventing and treating *H. pylori* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *H. pylori* infection by stimulating humoral and/or cell-mediated immunity against *H. pylori*. It should be understood that amelioration of any of the symptoms of *H. pylori* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *H. pylori*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

Determination of candidate protein antigens for antibody and vaccine development

The selection of candidate protein antigens for vaccine development were derived from the nucleotide sequence. First, all possible open reading frames (ORF's) greater than 50 nucleotides in all six reading frames were identified and translated into amino acid sequences. Second, the identified ORF's were analyzed for homology to other known exported or membrane proteins and the ORF's were also analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches were performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities better than 1x10 (ee-6)) to membrane or exported proteins represent likely protein antigens for vaccine development. Possible functions are provided to some of the *H. pylori* genes as indicated in Figure 560 based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) was used to examine the ORF amino acid sequences using our own software. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties

of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Infrequently it is not possible to distinguish between multiple possible nucleotides at a given position in the nucleic acid sequence. In those cases the ambiguities are denoted by an extended alphabet as follows:

These are the official IUPAC-IUB single-letter base codes

Code	Base Description	
G	Guanine	
A	Adenine	
T	Thymine	
C	Cytosine	
R	Purine	(A or G)
Y	Pyrimidine	(C or T or U)
M	Amino	(A or C)
K	Ketone	(G or T)
S	Strong interaction	(C or G)
W	Weak interaction	(A or T)
H	Not-G	(A or C or T)
B	Not-A	(C or G or T)
V	Not-T (not-U)	(A or C or G)
D	Not-C	(A or G or T)
N	Any	(A or C or G or T)

The amino acid translations of this invention account for the ambiguity in the nucleic acid sequence by translating the ambiguous codon as the letter "X". In all cases, the permissible amino acid residues at a position are clear from an examination of the nucleic acid sequence based on the standard genetic code.

Production of Fragments and Analogs

The inventor has discovered novel gene products, e.g. bacterial surface gene products, from the organism *H. pylori*. Once an example of this core structure has been provided one skilled in the art can alter the disclosed structure (of *H. pylori* genes), e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of prior art methods which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogues of cellular proteins for the ability to bind *H. pylori* polypeptides. Such screens are useful for discovery of inhibitors of *H. pylori*.

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNA's which encode an array of fragments. DNA's which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Production of Altered DNA and Peptide Sequences: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). This is a very powerful and relatively rapid method of introducing random mutations. The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and

essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Production of Altered DNA and Peptide Sequences: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site

for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci.* USA, 75: 5765[1978]).

Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are compatible with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

Primary High-Through-Put Methods for Screening Libraries of Peptide Fragments or Homologs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *H. pylori* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

Two Hybrid Systems

Two hybrid assays such as the system described above (as with the other screening methods described herein), can be used to identify polypeptides, e.g.,fragments or analogs of a naturally-occurring *H. pylori* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *H. pylori* protein. (The *H. pylori* domain is used as the bait protein and the library of variants are expressed as fish fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *H. pylori* polypeptide.

Display Libraries

In one approach to screening assays, the candidate peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS*

18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages M13, fd., and f1 are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH_2-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines 91*, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motile organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus*

protein A and the outer membrane protease IgA of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to

different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7-10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

Secondary Screens

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art

to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine to perform for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics

The invention also provides for reduction of the protein binding domains of the subject *H. pylori*-like family polypeptides, e.g., an *H. pylori* polypeptide, to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a *H. pylori* to its counter ligand, e.g., in the case of an *H. pylori* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *H. pylori* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *H. pylori*-derived peptidomimetics which competitively or noncompetatively inhibit binding of the *H. pylori* polypeptide with an interacting polypeptide (see, for example, "Peptide inhibitors of human papillomavirus protein binding to retinoblastoma gene protein" European patent applications EP-412,762A and EP-B31,080A). For example, scanning mutagenesis can be used to map the amino acid residues of a particular *H. pylori* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *H. pylori* polypeptide to an interacting polypeptide and thereby interfere with the function of *H. pylori* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gama lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun*126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

Kits

The nucleic acid, peptides and antibodies of the present invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, peptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose.

Exemplification

1. Cloning and Sequencing of *H. pylori* DNA

H. pylori chromosomal DNA was isolated according to a basic DNA protocol outlined in Schleif R.F. and Wensink P.C., *Practical Methods in Molecular Biology*, p.98, Springer-Verlag, NY., 1981, with minor modifications. Briefly, cells were pelleted, resuspended in TE (10 mM Tris, 1 mM EDTA, pH 7.6) and GES lysis buffer (5.1 M guanidium thiocyanate, 0.1 M EDTA, pH 8.0, 0.5% N-laurylsarcosine) was added. Suspension was chilled and ammonium acetate (NH_4Ac) was added to final concentration of 2.0 M. DNA was extracted, first with chloroform, then with phenol-chloroform, and reextracted with chloroform. DNA was precipitated with isopropanol, washed twice with 70% EtOH, dried and resuspended in TE.

Following isolation whole genomic *H. pylori* DNA was nebulized (Bodenteich et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994) to a median size of 2000 bp. After nebulization, the DNA was concentrated and separated on a standard 1% agarose gel. Several fractions, corresponding to approximate sizes 900-1300 bp, 1300-1700 bp, 1700-2200 bp, 2200-2700 bp, were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complimentary to the BstXI-cut pMPX vectors, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector religate itself easily. The linker-adopted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to each of the 20 pMPX vectors to construct a series of

"shotgun" subclone libraries. The vectors contain an out-of-frame lacZ gene at the cloning site which becomes in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their blue-color.

All subsequent steps were based on the multiplex DNA sequencing protocols outlined in Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988. Only major modifications to the protocols are highlighted. Briefly, each of the 20 vectors was then transformed into DH5α competent cells (Gibco/BRL, DH5α transformation protocol). The libraries were assessed by plating onto antibiotic plates containing ampicillin, methicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and pooling into the multiplex pools. The clones were picked and pooled into 40 ml growth medium cultures. The cultures were grown overnight at 37°C. DNA was purified using the Qiagen Midi-prep kits and Tip-100 columns (Qiagen, Inc.). In this manner, 100 μg of DNA was obtained per pool. 15 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy with 250-300 base average read-lengths.

These purified DNA samples were then sequenced using the multiplex DNA sequencing based on chemical degradation methods (Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988) or by Sequithrem (Epicenter Technologies) dideoxy sequencing protocols. The sequencing reactions were electrophoresed and transferred onto nylon membranes by direct transfer electrophoresis from 40 cm gels (Richterich P. and Church G.M., *Methods in Enzemology* 218:187-222, 1993) or by electroblotting (Church, *supra*). 24 samples were run per gel. 45 successful membranes were produced by chemical sequencing and 8 were produced by dideoxy sequencing. The DNA was covalently bound to the membranes by exposure to ultraviolet light, and hybridized with labeled oligonucleotides complimentary to tag sequences on the vectors (Church, *supra*). The membranes were washed to rinse off non-specifically bound probe, and exposed to X-ray film to visualize individual sequence ladders. After autoradiography, the hybridized probe was removed by incubation at 65°C, and the hybridization cycle repeated with another tag sequence until the membrane has been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes. Thus, each gel produced a large number of films, each containing new sequencing information. Whenever a new blot was processed, it was initially probed for an internal standard sequence added to each of the pools.

Digital images of the films were generated using a laser-scanning densitometer (Molecular Dynamics, Sunnyvale, CA). The digitized images were processed on computer workstations (VaxStation 4000's) using the program REPLICA™ (Church et al., *Automated DNA Sequenicng and Analysis* (J.C. Venter, ed.), Academic Press, 1994).

Image processing included lane straightening, contrast adjustment to smooth out intensity differences, and resolution enhancement by iterative gaussian deconvolution. The sequences were then automatically picked in REPLICA™ and displayed for interactive proofreading before being stored in a project database. The proofreading was accomplished by a quick visual scan of the film image followed by mouse clicks on the bands of the displayed image to modify the base calls. For typical sequences derived by chemical sequencing, the error rate of the REPLICA™ base calling software was 2-5% with most errors occurring near the end of a sequence read. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received a number correspond to (microtiter plate and probe information) and lane set number (corresponding to microtiter plate columns). This number serves as a permanent identifier of the sequence so it is always possible to identify the original of any particular sequence without recourse to a specialized database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequenicng and Analysis* (J.C. Venter, ed.), Academic Press, 1994). This program has proven to be fast and reliable for most sequences. The assembled contigs were displayed using a modified version of GelAssemble, developed by the Genetics Computer Group (GCG) (Devereux et al., *Nucleic Acid Res.* 12:387-95, 1984) that interacts with REPLICA™. This provided for an integrated editor that allows multiple sequence gel images to be instantaneously called up from the REPLICA™ database and displayed to allow rapid scanning of contigs and proofreading of gel traces where discrepancies occurred between different sequence reads in the assembly.

II. Identification, cloning and expression of recombinant *H. pylori* DNA sequences

To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori* a powerful gene expression system, the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, was selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, was fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end was selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above was ppiB, a gene cloned for use as a control in the expression studies. In this study, the sequence for *H. pylori* ppiB contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene does not contain a signal sequence and is expressed as a cytosolic protein.

PCR Amplification and cloning of DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.

Sequences chosen (from the list of the DNA sequences of the invention) for cloning from the J99 strain of *H. pylori* were prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers (Table 2) specific for the 5' and 3' ends of open reading frames (ORFs) were designed and purchased (GibcoBRL Life Technologies, Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) were designed to include an NcoI cloning site at the extreme 5' terminus, except for *H. pylori* sequence 4821082 (SEQ ID NO: 212) where NdeI was used. These primers were designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *H. pylori* DNA sequence. An exception is *H. pylori* sequence 4821082 (SEQ ID NO: 212) where the initiator methionine is immediately followed by the remainder of the native *H. pylori* DNA sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) included a EcoRI site at the extreme 5' terminus to permit cloning of each *H. pylori* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag. An exception to the above, as noted earlier, is the vector construction for the ppiB gene. A synthetic oligonucleotide primer specific for the 5' end of ppiB gene encoded a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encoded a XhoI site at its extreme 5' terminus.

TABLE 2

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences

Outer membrane Proteins	**Forward primer 5' to 3'**	**Reverse Primer 5' to 3'**
7116626 (SEQ ID NO: 223)	5'-ATATCCATGGTGAGT TTGATGA-3' (SEQ ID NO:229)	5'-ATGAATTCAATTTTT TATTTTGCCA-3' (SEQ ID NO:230)
29479681 (SEQ ID NO: 179)	5'-AATTCCATGGTGGGG GCTATG-3' (SEQ ID NO:231)	5'-ATGAATTCTCGATAG CCAAAATC-3' (SEQ ID NO:232)
Periplasmic/ Secreted Proteins		
30100332 (SEQ ID NO: 181)	5'-ATTTCCATGGTCATG TCTCATATT-3' (SEQ ID NO:233)	5'-ATGAATTCCATCTTT TATTCCAC-3' (SEQ ID NO:234)
4721061 (SEQ ID NO: 211)	5'-AACCATGGTGATTT TAAGCATTGAAAG-3' (SEQ ID NO:235)	5'-AAGAATTCCACTCA AAATTTTTTAACAG-3' (SEQ ID NO:236)

Other Surface Proteins		
4821082 (SEQ ID NO: 212)	5'-GATCATCCATATGTT ATCTTCTAAT-3' (SEQ ID NO:237)	5'-TGAATTCAACCATTT TAACCCTG-3' (SEQ ID NO:238)
978477 (SEQ ID NO: 228)	5'-TATACCATGGTGAA ATTTTTTCTTTTA-3' (SEQ ID NO:239)	5'-AGAATTCAATTGCG TCTTGTAAAAG-3' (SEQ ID NO:240)
Cytoplasmic Protein		
ppiB	5'-TTATGGATCCAAAC CAATTAAAACT-3' (SEQ ID NO:241)	5'-TATCTCGAGTTATA GAGAAGGGC-3' (SEQ ID NO:242)

Genomic DNA prepared from the J99 strain of *H. pylori* (ATCC #55679) was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) was introduced into a reaction vial containing 2 mM $MgCl_2$, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters. The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Sequences 7116626 (SEQ ID NO: 223), 29479681 (SEQ ID NO: 179), 30100332 (SEQ ID NO: 181), 4821082 (SEQ ID NO: 212) and 978477 (SEQ ID NO: 228);
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequence 4721061 (SEQ ID NO: 211);
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 36°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 60°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Conditions for amplification of *H. pylori* ppiB;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 32°C for 15 sec and 72°C for 1.5 min
25 cycles at 94°C for 15 sec, 56°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes

Upon completion of thermal cycling reactions, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples were subjected to digestion with the restriction endonucleases, NcoI and EcoRI (New England BioLabs, Beverly, MA, USA), or in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 212), with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of H. pylori DNA sequences into the pET-28b prokaryotic expression vector.

The pET-28b vector was prepared for cloning by digestion with NcoI and EcoRI, or in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 212) with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). In the case of cloning ppiB, the pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, was used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.

Following digestion, DNA inserts were cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector, except for the amplified insert for ppiB, which was cloned into the pET-28a expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction was mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl2, 10 mM MgSO4 and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts as described below.

Identification of recombinant pET expression plasmids carrying H. pylori sequences

Individual BL21 clones transformed with recombinant pET-28b-H.pylori ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression of recombinant H. pylori sequences in E. coli

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying a T7 promoter and a gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *H. pylori* sequences, 50 nanograms of plasmid DNA isolated as described above was used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) was expressed in the pET-System as described for the *H. pylori* recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour, and the culture was then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nM of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1

mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

III. Purification of recombinant proteins from *E. coli*

Analytical Methods

The concentrations of purified protein preparations were quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels (12% or 4.0 to 25 % acrylamide gradient gels) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers included rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

1. Purification of soluble proteins

All steps were carried out at 4°C. Frozen cells were thawed, resuspended in 5 volumes of lysis buffer (20 mM Tris, pH 7.9, 0.5 M NaCl, 5 mM imidazole with 10% glycerol, 0.1 % 2-mercaptoethanol, 200 µg/ ml lysozyme, 1 mM phenylmethylsulfonyl fluoride (PMSF), and 10 ug/ml each of leupeptin, aprotinin, pepstatin, L-1-chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate was made 0.1 % Brij 35, and centrifuged at 100,000 x g for 1 hour to yield a clear supernatant (crude extract).

Following filtration through a 0.8 µm Supor filter (Gelman Sciences, FRG) the crude extract was loaded directly onto a Ni^{2+}- nitrilotriacetate-agarose (NTA) with a 5 milliliter bed volume (Hochuli, E., Dbeli, H., and Schacheer, A. (1987) J. Chromatography 411, 177-184) pre-equilibrated in lysis buffer containing 10 % glycerol, 0.1 % Brij 35 and 1 mM PMSF. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol, 0.1 % Brij 35, and was eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD_{280} nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

Recombinant beta-galactosidase (lacZ) and peptidyl-prolyl cis-trans isomerase (ppiB)

Fractions containing the recombinant proteins from the Ni^{2+}-NTA-agarose columns were pooled and then concentrated to approximately 5 ml by centrifugal filtration (Centriprep-10, Amicon, MA), and loaded directly onto a 180-ml column (1.6 X 91 cm) of Sephacryl S-100 HR gel filtration medium equilibrated in Buffer A (10 mM Hepes, pH 7.5, 150 mM NaCl, 0.1 mM EGTA) and run in Buffer A at 18 ml/h. Fractions containing the recombinant protein were identified by absorbance at 280 nm and analyzed by SDS-PAGE. Fractions were pooled and concentrated by centrifugal filtration.

Recombinant protein 7116626 (SEQ ID NO: 223)

Fractions containing the recombinant protein from the Ni^{2+} -NTA-agarose column were pooled and dialyzed overnight against 1 liter of dialysis buffer (10 mM MOPS, pH 6.5, 50 mM NaCl, 0.1 mM EGTA, 0.02% Brij 35 and 1 mM PMSF). In the morning, a fine white precipitate was removed by centrifugation and the resulting supernatant was loaded onto an 8 ml (8 x 75 mm) MonoS high performance liquid chromatography column (Pharmacia Biotechnology, Inc., Piscataway, NJ, USA) equilibrated in buffer B (10 mM MOPS, pH 6.5, 0.1 mM EGTA) containing 50 mM NaCl. The column was washed with 10 bed volumes of buffer B containing 50 mM NaCl, and developed with a 50-ml linear gradient of increasing NaCl (50 to 500 mM). Recombinant protein 7116626 (SEQ ID NO: 223) eluted as a sharp peak at 300 mM NaCl.

2. Purification of insoluble proteins from inclusion bodies

The following steps were carried out at 4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % -mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets were washed with lysis buffer containing 10 % glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% -mercaptoethanol, followed by several washes with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol. The resulting white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials..

Recombinant proteins 30100332 (SEQ ID NO: 181), 4721061 (SEQ ID NO: 211)

The following steps were carried out at room temperature. Purified inclusion bodies were dissolved in 20 ml 8.0 M urea in lysis buffer with 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not dissolve were removed by centrifugation. The clear supernatant was filtered, then loaded onto a Ni^{2+} -NTA agarose column pre-equilibrated in 8.0 M urea in Lysis Buffer. The

column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1.0 mM PMSF and 0.1 % 2-mercaptoethanol, and developed with sequential steps of lysis buffer containing 8M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD_{280} nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

Recombinant proteins 29479681 (SEQ ID NO: 179), 978477 (SEQ ID NO: 228)

The pellet containing the inclusion bodies was solubilized in buffer B containing 8 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated for 1 hour at room temperature. Insoluble materials were removed by centrifugation at 20,000 x g for 30 min, and the cleared supernatant was loaded onto a 15 ml (1.6 x 7.5 cm) SP-Sepharose column pre-equilibrated in buffer B, 6 M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol. After washing the column with 10 bed volumes, the column was developed with a linear gradient from 0 to 500 mM NaCl.

Dialysis and concentration of protein samples

Urea was removed slowly from the protein samples by dialysis against Tris-buffered saline (TBS; 10 mM Tris pH 8.0, 150 mM NaCl) containing 0.5 % deoxycholate (DOC) with sequential reduction in urea concentration as follows; 6M, 4M, 3M, 2M, 1M, 0.5 M and finally TBS without any urea. Each dialysis step was conducted for a minimum of 4 hours at room temperature.

After dialysis, samples were concentrated by pressure filtration using Amicon stirred-cells. Protein concentrations were measured using the methods of Perkins (1986 Eur. J. Biochem. 157, 169-180), Bradford ((1976) Anal. Biochem. 72, 248-254) and Lowry ((1951) J. Biol. Chem. 193, pages 265-275).

The recombinant proteins purified by the methods described above are summarized in Table 3 below.

TABLE 3

J99 Sequence Identifier	Homolog identified by Blast	Gene symbol of Homolog	Baccterial fraction used to purify recombinant proteins	Method of purification	Relative MW on SDS-PAGE gel	Final Con-centration of purified protein	Composition of buffer
Outer Membrane Proteins							
7116626 (SEQ ID NO: 223)	P26093	**e(P4)**	Soluble fraction	His-Tag	29 kDa	0.8 mg/ml	A
						1.85 mg/ml	C
29479681 (SEQ ID NO: 179)	P13036	**fecA**	Inclusions bodies	SP-Sepharose	23 kDa	2.36 mg/ml	B

						0.5 mg ml	B
						----	as dry pellet
				gel filtration S100 HR			
Periplasmic/Secreted Protein							
3010032 (SEQ ID NO: 181)	P23847	**dppA**	Inclusion bodies	His-Tag	11 kDa	2.88 mg/ml	B
4721061 (SEQ ID NO: 211)	P36175	**GCP**	Inclusion bodies	His-Tag	38 kDa	2.8 mg/ml	B
Other Surface Proteins							
4821082 (SEQ ID NO:212)	P08089	**M protein**	Inclusion bodies	His-Tag	20 kDa	1.16 mg/ml	B
978477 (SEQ ID NO: 228)	L28919	**FBP54**	Inclusion bodies	SP-Sepharose	44 kDa	2.56 mg/ml	B
						0.3 mg/ml	B
Control Proteins with His-Tag							
	P00722	**lacZ**	Soluble fraction	His-Tag	116 kDa	10 mg/ml	A
				gel filtration S200 HR			
		ppiB	Soluble fraction	His-Tag	21 kDa	4.4 mg/ml	A
				gel filtration S100 HR			

Buffer compositions:
A=10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA
B= 10 mM Tris pH 8.0, 150 mM NaCl, 0.5 % DOC
C= 10 mM MOPS pH 6.5, 300 mM NaCl, 0.1 EGTA

IV. Analysis of *H. pylori* proteins as Vaccine candidates

To investigate the immunomodulatory effect of *H. pylori* proteins, a mouse/*H. pylori* model was used. This model mimics the human *H. pylori* infection in many respects. The focus is on the effect of oral immunization in *H. pylori* infected animals in order to test the concept of therapeutic oral immunotherapy.

Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding center (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. The animals were 4-6 weeks old at arrival.

Infection

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain (VacA negative) of *H. pylori* (strain AH244, originally isolated from an ulcer patient). In our hands, this strain has earlier proven to be a good colonizer of the mouse stomach. The bacteria were grown overnight in Brucella broth supplemented with 10 % fetal calf serum, at 37°C in a microaerophilic atmosphere (10% CO_2, 5%O_2). The animals

were given an oral dose of omeprazole (400 μmol/kg) and 3-5 h after this an oral inoculation of *H. pylori* in broth (approximately 10^8 cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

Recombinant *H. pylori* antigens were chosen based on their association with externally exposed *H. pylori* cell membrane. These antigens were selected from the following groups: (1.) Outer Membrane Proteins; (2.) Periplastic/Secreted proteins; (3.) Outer Surface proteins; and (4.) Inner Membrane proteins. All recombinant proteins were constructed with a hexa-HIS tag for purification reasons and the non-*Helicobacter pylori* control protein (β-galactosidase from *E. coli*; LacZ), was constructed in the same way.

All antigens were given in a soluble form, i.e. dissolved in either a HEPES buffer or in a buffer containing 0.5% Deoxycholate (DOC).

The antigens are listed in Table 4 below.

Table 4
Helicobacter pylori proteins

Outer membrane Proteins
SEQ ID NO:179
SEQ ID NO:223

Periplastic/Secreted proteins
SEQ ID NO:181
SEQ ID NO:211

Other cell envelope proteins
SEQ ID NO:212
SEQ ID NO:228

Control proteins
β-galactosidase (LacZ)

Immunizations

Ten animals in each group were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified antigens in solution or suspension were given at a dose of 100 μg/mouse. As an adjuvant, the animals were also given 10 μg/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 μmol/kg) was given orally to the animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Infected control animals received HEPES buffer + CT or DOC buffer + CT. Animals were sacrificed 2-4 weeks after final immunization. A general outline of the study is shown in Table 5 below.

Table 5
Study outline, therapeutic immunization:

Mice were all infected with *H. pylori* strain AH244 at day 30. Proteins are listed by their Seq ID #'s.

Substance	Mouse strain n=10	Dose/mouse	Dates for dosing
1. Controls, PBS	Balb/c	0.3 ml	0, 14, 24, 34
2. Cholera toxin, 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
3. Protein 179, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
4. Protein 181, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
5. Protein 211, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
6. Protein 212, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
7. Protein 228, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34
8. Protein 223, 100 μg + CT 10 μg	Balb/c	0.3 ml	0, 14, 24, 34

Analysis of infection

Mucosal infection: The mice were sacrificed by CO_2 and cervical dislocation. The abdomen was opened and the stomach removed. After cutting the stomach along the greater curvature, it was rinsed in saline. The mucosa from the antrum and corpus of an area of $25mm^2$ was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth and plated onto Blood Skirrow selective plates. The plates were incubated under microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.

The urease test was performed essentially as follows. The reagent, Urea Agar Base Concentrate, was purchased from DIFCO Laboratories, Detroit, MI (Catalog # 0284-61-3). Urea agar base concentrate was diluted 1:10 with water. 1 ml of the diluted concentrate was mixed with 100-200 μl of actively growing *H. pylori* cells. Color change to magenta indicated that cells were urease positive.

The catalase test was performed essentially as follows. The reagent, N,N,N',N'-Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the reagent (1% w/v in water) was prepared. *H. pylori* cells were swabbed onto Whatman filter paper and overlaid with the 1% solution. Color change to dark blue indicated that the cells were catalase positive.

Serum antibodies: From all mice serum was prepared from blood drawn by heart puncture. Serum antibodies were identified by regular ELISA techniques, where the specific antigens of *Helicobacter pylori* were plated.

Mucosal antibodies: Gentle scrapings of a defined part of the corpus and of 4 cm of duodenum were performed in 50% of the mice in order to detect the presence of antibodies

in the mucous. The antibody titers were determined by regular ELISA techniqc as for serum antibodies.

Statistical analysis: Wilcoxon-Mann-Whitney sign rank test was used for determination of significant effects of the antigens on *Helicobacter pylori* colonization. $P<0.05$ was considered significant. Because the antrum is the major colonization site for *Helicobacter* most emphasis was put upon changes in the antral colonization.

Results

Antibodies in sera: All antigens tested given together with CT gave rise to a measurable specific titer in serum. The highest responses were seen with SEQ ID NOs:223, 211, and 212 (see Figure 2).

Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with SEQ ID NOs:181, followed by 223 (see Figure 3).

Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain AH244) in both antrum and corpus of the stomach. Of the antigens tested 2 proteins (SEQ ID NOs: 211 and 212) gave a good and significant reduction and/or eradication of the *H. pylori* infection. The degree of colonization of the antrum was lower following immunization with SEQ ID NOs: 228 and 223 compared to control. The effect of SEQ ID NOs:179, and 181 did not differ from control. The control protein lacZ, i.e. the non-*H. pylori* protein, had no eradication effect and in fact had higher *Helicobacter* colonization compared to the HEPES + CT control. All data are shown in Figures 4 and 5 for proteins dissolved in HEPES and DOC respectively. Data is shown as geometric mean values. n=8-10 Wilcoxon-Mann-Whitney sign rank test * = $p<0.05$; x/10 = number of mice showing eradication of *H. pylori* over the total number of mice examined.

The data presented indicate that all of the *H. pylori* associated proteins included in this study, when used as oral immunogens in conjunction with the oral adjuvant CT, resulted in stimulation of an immune response as measured by specific serum and mucosal antibodies. A majority of the proteins led to a reduction, and in some cases complete clearance of the colonization of *H. pylori* in this animal model. It should be noted that the reduction or clearance was due to heterologous protection rather than homologous protection (the polypeptides were based on the *H. pylori* J99 strain sequence and used in the therapeutic immunization studies against a different (AH244) challenge strain), indicating the vaccine potential against a wide variety of *H. pylori* strains.

The highest colonization in the antrum was seen in animals treated with the non-*Helicobacter* protein LacZ, indicating that the effects seen with the *Helicobacter pylori* antigens were specific.

Taken together these data strongly support the use of these *H. pylori* proteins in a pharmaceutical formulation for the use in humans to treat and/or prevent *H. pylori* infections.

V. Sequence Variance Analysis of genes in *Helicobacter pylori* strains

Three genes were cloned and sequenced from several strains of *H. pylori* to compare the DNA and deduced amino acid sequences. This information was used to determine the sequence variation between the *H. pylori* strain, J99, and other *H. pylori* strains isolated from human patients.

Preparation of Chromosomal DNA.

Cultures of *H. pylori* strains (as listed in Table 8) were grown in BLBB (1% Tryptone, 1% Peptamin 0.1% Glucose, 0.2% Yeast Extract 0.5% Sodium Chloride, 5% Fetal Bovine Serum) to an OD_{600} of 0.2. Cells were centrifuged in a Sorvall RC-3B at 3500 x g at 4°C for 15 minutes and the pellet resuspended in 0.95 mls of 10 mM Tris-HCl, 0.1 mM EDTA (TE). Lysozyme was added to a final concentration of 1mg/ml along with SDS to 1% and RNAse A + T1 to 0.5mg/ml and 5 units/ml respectively, and incubated at 37°C for one hour. Proteinase K was then added to a final concentration of 0.4mg/ml and the sample was incubated at 55°C for more than one hour. NaCl was added to the sample to a concentration of 0.65 M, mixed carefully, and 0.15 ml of 10% CTAB in 0.7M NaCL (final is 1% CTAB/70mM NaCL) was added followed by incubation at 65°C for 20 minutes. At this point, the samples were extracted with chloroform:isoamyl alcohol, extracted with phenol, and extracted again with chloroform:isoamyl alcohol. DNA was precipitated with either EtOH (1.5 x volumes) or isopropanol (0.6 x volumes) at -70°C for 10 minutes, washed in 70% EtOH and resuspended in TE.

PCR Amplification and cloning.

Genomic DNA prepared from twelve strains of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (10 nanograms) was introduced into a reaction vial containing 2 mM $MgCl_2$, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 6) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 0.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 20 microliters in duplicate reactions.

Table 6

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
SEQ ID NO:223	5'-ATATCCATGGTGAGTTTGA TGA-3' (SEQ ID NO:243)	5'-ATGAATTCAATTTTTTATTTT GCCA-3' (SEQ ID NO:244)
SEQ ID NO:179	5'-AATTCCATGGCTATCCAAAT CCG-3' (SEQ ID NO:245)	5'-ATGAATTCGCCAAAATCGTA GTATT-3' (SEQ ID NO:246)
SEQ ID NO:199	5'-GATACCATGGAATTTATGAA AAAG-3' (SEQ ID NO:247)	5'-TGAATTCGAAAAAGTGTAGT TATAC-3' (SEQ ID NO:248)

The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Sequences (by SEQ ID NO:) 223 and 199;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.

Sequences (by SEQ ID NO:) 179;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 20 sec and 72°C for 2 min
25 cycles at 94°C for 15 sec, 55°C for 20 sec and 72°C for 2 min
Reactions were concluded at 72°C for 8 minutes.

Upon completion of thermal cycling reactions, each pair of samples were combined and used directly for cloning into the pCR cloning vector as described below.

Cloning of H. pylori DNA sequences into the pCR TA cloning vector.

All amplified inserts were cloned into the pCR 2.1 (pCRII in the case of *H. pylori* sequence 223) vector by the method described in the Original TA cloning kit (Invitrogen, San Diego, CA). Products of the ligation reaction were then used to transform the TOP10F' (INVaF' in the case of *H. pylori* sequence 223) strain of *E. coli* as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E coli* strain TOP10F' or *E. coli* strain INVaF' were transformed with recombinant pCR expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). Briefly, 2 microliters of 0.5 micromolar BME was added to each vial of 50 microliters of competent cells.

Subsequently, 2 microliters of ligation reaction was mixed with the competent cells and incubated on ice for 30 minutes. The cells and ligation mixture were then subjected to a "heat shock" at 42°C for 30 seconds, and were subsequently placed on ice for an additional 2 minutes, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl2, 10 mM MgSO4 and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate or 100 micrograms/ml ampicillan for growth overnight. Transformed colonies of TOP10F' or INVaF' were then picked and analyzed to evaluate cloned inserts as described below.

Identification of recombinant PCR plasmids carrying H. pylori sequences

Individual TOP10F' or INVaF' clones transformed with recombinant pCR-*H.pylori* ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the cloning vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994).

Individual clones of recombinant pCR vectors carrying properly cloned *H. pylori* ORFs were picked for sequence analysis. Sequence analysis was performed on ABI Sequencers using standard protocols (Perkin Elmer) using vector-specific primers (as found in PCRII or pCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific to the ORF as listed in Table 7 below.

Table 7
Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	**Forward primers 5' to 3'**	**Reverse Primers 5' to 3'**
SEQ ID NO:223	5'-TTGAACACTTTTGATTATGCGG-3' (SEQ ID NO:249) 5'-GGATTATGCGATTGTTTTACAAG-3' (SEQ ID NO:250)	5'-GTCTTTAGCAAAAATGGCGTC-3' (SEQ ID NO:251) 5'-AATGAGCGTAAGAGAGCCTTC-3' (SEQ ID NO:252)
SEQ ID NO:179	5'-CTTATGGGGGTATTGTCA-3' (SEQ ID NO:253) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:254)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:255) 5'-CTGCCTCCACCTTTGATC-3' (SEQ ID NO:256)
SEQ ID NO:199	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:257) 5'-ACTTGGAAAAGCTCTGCA-3' (SEQ ID NO:258)	5'-CTTGCTTGTCATATCTAGC-3' (SEQ ID NO:259) 5'-GTTGAAGTGTTGGTGCTA-3' (SEQ ID NO:260)

	5'-CAAGCAAGTGGTTTGGTTTTAG-3' (SEQ ID NO:261) 5'-TGGAAAGAGCAAATCATTGAAG-3' (SEQ ID NO:262)	5'-GCCCATAATCAAAAAGCCCAT-3' (SEQ ID NO:263) 5'-CTAAAACCAAACCACTTGCT TGTC-3' (SEQ ID NO:264)
Vector Primers	5'-GTAAAACGACGGCCAG-3' (SEQ ID NO:265)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:266)

Results

The PCR error rate for the experiments described herein was determined to be 2 base changes out of 4485 bases, which is equivalent to an estimated error rate of less than or equal to 0.04%.

DNA sequence analysis was performed on four different open reading frames identified as genes and amplified by PCR methods from a dozen different strains of the bacterium *Helicobacter pylori*. The deduced amino acid sequences of three of the four open reading frames that were selected for this study showed statistically significant BLAST homology to defined proteins present in other bacterial species. Those ORFs included: SEQ ID NO:223, homologous to lipoprotein e (P4) present in the outer membrane of H. influenzae; SEQ ID NO:179, homologous to fecA, an outer membrane receptor in iron (III) dicitrate transport in *E. coli*. SEQ ID NO:199 was identified as an unknown open reading frame, because it showed low homology with sequences in the public databases.

To assess the extent of conservation or variance in the ORFs across various strains of *H. pylori*, changes in DNA sequence and the deduced protein sequence were compared to the DNA and deduced protein sequences found in the J99 strain of *H. pylori* (*see* Table 8 below). Results are presented as percent identity to the J99 strain of *H. pylori* sequenced by random shotgun cloning. To control for any variations in the J99 sequence each of the four open reading frames were cloned and sequenced again from the J99 bacterial strain and that sequence information was compared to the sequence information that had been collected from inserts cloned by random shotgun sequencing of the J99 strain.

Table 8
Multiple Strain DNA Sequence analysis of H. pylori Vaccine Candidates

J99 Seq. ID #:	223	223	179	179	199	199
Length of Region Sequenced:	232 a.a.	696 nt.	182 a.a.	548 nt.	273 a.a.	819 nt.
Strain Tested	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. Identity
J99	100.00%	100.00%	100.00%	100.00%	99.63%	99.88%
AH244	n.d.	n.d.	99.09%	96.71%	98.90%	96.45%
AH4	97.84%	95.83%	n.d.	n.d.	97.80%	95.73%
AH5	98.28%	96.12%	98.91%	96.90%	98.53%	95.73%
AH15	97.41%	95.98%	99.82%	97.99%	99.63%	96.09%
AH61	97.84%	95.98%	99.27%	97.44%	n.d.	n.d.
5155	n.d.	n.d.	99.45%	97.08%	98.53%	95.60%
5294	98.28%	95.40%	99.64%	97.26%	97.07%	95.48%
7958	97.84%	95.40%	n.d.	n.d.	99.63%	96.46%
5640	97.41%	95.69%	99.09%	97.63%	98.53%	95.48%
AH18	98.71%	95.69%	99.64%	97.44%	100.00%	95.97%
AH24	97.84%	95.40%	99.27%	96.71%	100.00%	96.46%

n.d. = not done

VI. Experimental Knock-Out Protocol for the Determination of Essential *H. pylori* Genes as Potential Therapeutic Targets

Therapeutic targets are chosen from genes whose protein products appear to play key roles in essential cell pathways such as cell envelope synthesis, DNA synthesis, transcription, translation, regulation and colonization/virulence.

The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette in order to identify genes which are essential to the cell is modified from previously published methods (Labigne-Roussel et al., 1988, J. Bacteriology 170, pp. 1704-1708; Cover et al.,1994, J. Biological Chemistry 269, pp. 10566-10573; Reyrat et al., 1995, Proc. Natl. Acad. Sci. 92, pp 8768-8772). The result is a gene "knock-out."

Identification and Cloning of H. pylori Gene Sequences

The sequences of the genes or ORFs (open reading frames) selected as knock-out targets are identified from the *H. pylori* genomic sequence and used to design primers to specifically amplify the genes/ORFs. All synthetic oligonucleotide primers are designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and can be purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). If the ORF is smaller than 800 to 1000 base pairs, flanking primers are chosen outside of the open reading frame.

Genomic DNA prepared from the *Helicobacter pylori* HP-J99 strain (ATCC 55679) is used as the source of template DNA for amplification of the ORFs by PCR (polymerase chain reaction) (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). For the preparation of genomic DNA from *H. pylori*, see Example I. PCR amplification is carried out by introducing 10 nanograms of genomic HP-J99 DNA into a reaction vial containing 10 mM Tris pH 8.3, 50 mM KCl, 2 mM $MgCl_2$, 2 microMolar synthetic oligonucleotide primers (forward=F1 and reverse=R1), 0.2 mM of each deoxynucleotide triphosphate (dATP,dGTP, dCTP, dTTP), and 1.25 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 40 microliters. The PCR is carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers.

Upon completion of thermal cycling reactions, each sample of amplified DNA is visualized on a 2% TAE agarose gel stained with Ethidium Bromide (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) to determine that a single product of the expected size had resulted from the reaction. Amplified DNA is then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products are cloned into the pT7Blue T-Vector (catalog#69820-1, Novagen, Inc., Madison, WI, USA) using the TA cloning strategy (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The ligation of the PCR product into the vector is accomplished by mixing a 6 fold molar excess of the PCR product, 10 ng of pT7Blue-T vector (Novagen), 1 microliter of T4 DNA Ligase Buffer (New England Biolabs, Beverly, MA, USA), and 200 units of T4 DNA Ligase (New England Biolabs) into a final reaction volume of 10 microliters. Ligation is allowed to proceed for 16 hours at 16°C.

Ligation products are electroporated (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) into electroporation-competent XL-1 Blue or DH5-α *E.coli* cells (Clontech Lab., Inc. Palo Alto, CA, USA). Briefly, 1 microliter of ligation reaction is mixed with 40 microliters of electrocompetent cells and subjected to a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples are incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 10 mM $MgSO_4$ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples are then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100 microgram/ml IPTG. These plates are incubated overnight at 37°C. Ampicillin-resistant colonies with white color are selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA is isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

To verify that the correct *H.pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs are used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers used for the initial amplification of the J99 *H.pylori* sequence. Recognition of the primers and a PCR product of the correct size as visualized on a 2% TAE, ethidium bromide stained agarose gel are confirmation that the correct inserts had been cloned. Two to six such verified clones are obtained for each knock-out target, and frozen at -70°C for storage. To minimize errors due to PCR, plasmid DNA from these verified clones are pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs are again used to design a second pair of primers which flank the region of *H. pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but are oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones are used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers is away from each other, the portion of the ORF between the primers is not included in the resultant PCR product. The PCR product is a linear piece of DNA with *H. pylori* DNA at each end and the pT7Blue vector backbone between them which, in essence, results in the deletion of a portion of the ORFs. The PCR product is visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size has been amplified.

A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) is ligated to this PCR product by the TA cloning method used previously (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The Kanamycin cassette containing a *Campylobacter* kanamycin resistance gene is obtained by carrying out an EcoRI digestion of the recombinant plasmid pCTB8:*kan* (Cover et al.,1994, J. Biological Chemistry 269, pp. 10566-10573). The proper fragment (1.4 kb) is isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment is end repaired using the Klenow fill-in protocol, which involved mixing 4ug of the DNA fragment, 1 microliter of dATP,dGTP, dCTP, dTTP at 0.5 mM, 2 microliter of Klenow Buffer (New England Biolabs) and 5 units of Klenow DNA Polymerase I Large (Klenow) Fragment (New England Biolabs) into a 20 microliter reaction, incubating at 30°C for 15 min, and inactivating the enzyme by heating to 75°C for 10 minutes. This blunt-ended Kanamycin cassette is then purified through a Qiaquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The "T" overhang is then generated by mixing 5 micrograms of the blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM $MgCl_2$, 5 units of DNA Polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA), 20 microliters of 5 mM dTTP, in a 100 microliter reaction and incubating the reaction for 2 hours at 37°C. The "Kan-T" cassette is purified using a QIAquick column (Qiagen,

Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) is ligated to the Kan-T cassette by mixing 10 to 25 ng of deletion primer PCR product, 50 - 75 ng Kan-T cassette DNA, 1 microliter 10x T4 DNA Ligase reaction mixture, 0.5 microliter T4 DNA Ligase (New England Biolabs, Beverly, MA, USA) in a 10 microliter reaction and incubating for 16 hours at 16°C.

The ligation products are transformed into XL-1 Blue or DH5-α *E.coli* cells by electroporation as described previously. After recovery in SOC, cells are plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates are then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies have both the Ampicillin resistance gene present in the pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies are picked into LB containing 25 microgram/ml Kanamycin and plasmid DNA is isolated from the cultured cells using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

Several tests by PCR amplification are conducted on these plasmids to verify that the Kanamycin is inserted in the *H. pylori* gene/ORF, and to determine the orientation of the insertion of the Kanamycin-resistance gene relative to the *H. pylori* gene/ORF. To verify that the Kanamycin cassette is inserted into the *H. pylori* sequence, the plasmid DNAs are used as templates for PCR amplification with the set of primers originally used to clone the *H. pylori* gene/ORFs. The correct PCR product is the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. To avoid potential polar effects of the kanamycin resistance cassette on *H. pylori* gene expression, the orientation of the Kanamycin resistance gene with respect to the knock-out gene/ORF is determined and both orientations are eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers are designed from the ends of the kanamycin resistance gene ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3' (SEQ ID NO:267), and "Kan-2" 5'-AGACAGCAACATCTTTGTGAA-3' (SEQ ID NO:268)). By using each of the cloning primers in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H.pylori* sequence is determined. Positive clones are classified as either in the "A" orientation (the same direction of transcription is present for both the *H. pylori* gene and the Kanamycin resistance gene), or in the "B" orientation (the direction of transcription for the *H.pylori* gene is opposite to that of the Kanamycin resistance gene). Clones which share the same orientation (A or B) are pooled for subsequent experiments and independently transformed into *H. pylori*.

Transformation of Plasmid DNA into H. pylori cells

Two strains of *H. pylori* are used for transformation: HP-J99 (ATCC 55679), the clinical isolate which provided the DNA from which the *H. pylori* sequence database is

obtained, and AH244, an isolate which had been passaged in, and has the ability to colonize the mouse stomach. Cells for transformation are grown at 37°C, 10% CO_2, 100% humidity, either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells are grown to exponential phase, and examined microscopically to determine that the cells are "healthy" (actively moving cells) and not contaminated. If grown on plates, cells are harvested by scraping cells from the plate with a sterile loop, suspended in 1 ml of Brucella Broth, spun down (1 minute, top speed in eppendorf microfuge) and resuspended in 200 microliters Brucella Broth. If grown in Brucella Broth liquid, cells are centrifuged (15 minutes at 3000 rpm in a Beckman TJ6 centrifuge) and the cell pellet resuspended in 200 microliters of Brucella broth. An aliquot of cells is taken to determine the optical density at 600 nm, in order to calculate the concentration of cells. An aliquot (1 to 5 OD_{600} units/25 microliter) of the resuspended cells is placed onto a prewarmed Sheep-Blood agar plate, and the plate is further incubated at 37°C, 6% CO_2, 100% humidity for 4 hours. After this incubation, 10 microliters of plasmid DNA (100 micrograms per microliter) is spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene) and a negative control (no plasmid DNA) are done in parallel. The plates are returned to 37°C, 6% CO_2 for an additional 4 hours of incubation. Cells are then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO_2. Cells are then transferred to a Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin, and allowed to grow for 3 to 5 days at 37°C, 6% CO_2, 100% humidity. If colonies appear, they are picked and regrown as patches on a fresh Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR tests are done to verify that the colonies of transformants have arisen from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) is obtained by a rapid boiling DNA preparation method as follows. An aliquot of the colony (stab of the colony with a toothpick) is introduced into 100 microliters of 1% Triton X-100, 20 mM Tris, pH 8.5, and boiled for 6 minutes. An equal volume of phenol : chloroform (1:1) is added and vortexed. The mixture is microfuged for 5 minutes and the supernatant is used as DNA template for PCR with combinations of the following primers to verify homologous recombination at the proper chromosomal location.

TEST 1. PCR with cloning primers originally used to amplify the gene/ORF. A positive result of homologous recombination at the correct chromosomal location should show a single PCR product whose size is expected to be the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. A PCR product of just the size of the gene/ORF is proof that the gene had not been knocked out and that the transformant is not the result of homologous recombination at the correct chromosome location.

TEST 2. PCR with F3 (primer designed from sequences upstream of the gene/ORF and not present on the plasmid), and either primer Kan-1 or Kan-2 (primers designed from the ends of the kanamycin resistance gene), depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the location of F3 to the insertion site of kanamycin resistance gene). No PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

TEST 3. PCR with R3 (primer designed from sequences downstream of the gene/ORF and not present on the plasmid) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the insertion site of kanamycin resistance gene to the downstream location of R3). Again, no PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

Transformants showing positive results for all three tests above indicate that the gene is not essential for survival *in vitro*.

A negative result in any of the three above tests for each transformant indicates that the gene had not been disrupted, and that the gene is essential for survival *in vitro*.

In the event that no colonies result from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produces transformants, the plasmid DNA is further analyzed by PCR on DNA from transformant populations prior to plating for colony formation. This will verify that the plasmid can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA is incubated according to the transformation protocol described above. DNA is extracted from the *H. pylori* cells immediately after incubation with the plasmid DNAs and the DNA is used as template for the above TEST 2 and TEST 3. Positive results in TEST 2 and TEST 3 would verify that the plasmid DNA could enter the cells and undergo homologous recombination at the correct chromosomal location. If TEST 2 and TEST 3 are positive, then failure to obtain viable transformants indicates that the gene is essential, and cells suffering a disruption in that gene are incapable of colony formation

VII. High-throughput drug screen assay

Cloning, expression and protein purification

Cloning, transformation, expression and purification of the *H. pylori* target gene and its protein product,e.g., an *H. pylori* enzyme, to be used in a high-throughput drug screen assay, is carried out essentially as described in Examples II and III above. Development and application of a screening assay for a particular *H. pylori* gene product, peptidyl-propyl *cis-trans* isomerase, is described below as a specific example.

Enzymatic Assay

The assay is essentially as described by Fisher (Fischer, G., et.al. (1984) *Biomed. Biochim. Acta* 43:1101-1111). The assay measures the *cis-trans* isomerization of the Ala-Pro bond in the test peptide N-succinyl-Ala-Ala-Pro-Phe-p-nitroanilide (Sigma # S-7388, lot # 84H5805). The assay is coupled with α-chymotrypsin, where the ability of the protease to cleave the test peptide occurs only when the Ala-Pro bond is in *trans*. The conversion of the test peptide to the trans isomer in the assay is followed at 390 nm on a Beckman Model DU-650 spectophotometer. The data are collected every second with an average scanning of time of 0.5 second. Assays are carried out in 35 mM Hepes, pH 8.0, in a final volume of 400 ul, with 10 μM α-chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPIase. To initiate the reaction, 10 μl of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) is added to 390 μl of reaction mixture at room temperature.

Enzymatic assay in crude bacterial extract.

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth is harvested at mid-log phase ($OD_{600\ nm}$ ~ 1) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 μg/ml of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension is subjected to 3 cycles of freeze-thaw (15 minutes at -70 ^{o} C, then 30 minutes at room temperature), followed by sonication (three 20 second bursts). The lysate is centrifuged (12,000 g x 30 minutes) and the supernatant is assayed for enzymatic activity as described above.

Many *H. pylori* enzymes can be expressed at high levels and in an active form in *E. coli*. Such high yields of purified proteins provide for the design of various high throughput drug screening assays.

Other Embodiments

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridizes under high or low stringency conditions to a nucleic acid which encodes a polypeptide as shown in SEQ ID NOs:1-114 (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *H. pylori* polypeptides, especially by antisera to an active site or binding domain of *H. pylori* polypeptide

The invention also includes fragments, preferably biologically active fragments, or analogs of *H. pylori* polypeptides A biologically active fragment or analog is one having any *in vivo* or *in vitro* activity which is characteristic of the *H. pylori* polypeptides shown in

SEQ ID NOs:115-228, or of other naturally occurring *H. pylori* polypeptides, e.g., one or more of the biological activities described above. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO cells. Because peptides such as *H. pylori* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *H. pylori* fragment or *H. pylori* analog is one which exhibits a biological activity in any biological assay for *H. pylori* activity. Most preferably the fragment or analog possesses 10%, preferably 40%, or at least 90% of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

Analogs can differ from naturally occurring *H. pylori* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation.

Preferred analogs include *H. pylori* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not abolish the biological activity of the *H. pylori* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be taken from the table below.

TABLE 9
CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile,Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β-Ala Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val

Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-1-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met,D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met,D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met,D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to a *H. pylori* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *H. pylori* polypeptides can be generated by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *H. pylori* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *H. pylori* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

In order to obtain an *H. pylori* polypeptide, *H. pylori* polypeptide-encoding DNA can be introduced into an expression vector, the vector introduced into a cell suitable for expression of the desired protein, and the peptide recovered and purified, by prior art methods. Antibodies to the peptides an proteins can be made by immunizing an animal, e.g., a rabbit or mouse, and recovering anti-*H. pylori* polypeptide antibodies by prior art methods.

The nucleic acids and corresponding polypeptides of the invention were disclosed previously in the corresponding US application, U.S.S.N. 08/561,469, filed November 17, 1995 (Attorney Docket No.: GTN-001CP). The correlation between sequence identification numbers in the above-identified parent applications and sequence identification numbers provided herein is outlined in Table 10 below.

TABLE 10

Parent Nucleic Acid SEQ ID NO:	Relation -ship	New Nucleic Acid SEQ ID NO:	Parent Amino Acid SEQ ID NO:	Parent amino acid HPP #	Relation-ship	New Amino Acid SEQ ID NO:
881	a	1	385	2	a	115
882	a	2	390	9	a	116
883	a	3	401	20	a	117
884	a	4	407	26	a	118
885	a	5	409	28	a	119
886	a	6	410	29	a	120
887	a	7	413	34	a	121
888	a	8	431	55	a	122
889	a	9	435	60	a	123
890	a	10	442	68	a	124
891	a	11	445	71	a	125
892	a	12	449	75	a	126
893	a	13	463	89	a	127
894	a	14	464	90	a	128
895	a	15	467	94	a	129
896	a	16	470	97	a	130
897	a	17	474	101	a	131
898	a	18	476	103	a	132
899	a	19	477	104	a	133
900	a	20	480	107	a	134
901	a	21	485	114	a	135
902	a	22	487	116	a	136
903	a	23	502	133	a	137
904	a	24	507	139	a	138
905	a	25	508	140	a	139
906	a	26	511	144	a	140
907	a	27	515	148	a	141
908	a	28	517	150	a	142
909	a	29	521	154	a	143
910	a	30	526	161	a	144
911	a	31	534	170	a	145
912	a	32	538	175	a	146
913	a	33	541	178	a	147
914	a	34	545	183	a	148
915	a	35	549	187	a	149
916	a	36	551	189	a	150
917	a	37	552	190	a	151
918	a	38	557	195	a	152
919	a	39	559	197	a	153
920	a	40	561	199	a	154
921	a	41	569	209	a	155
922	a	42	571	211	a	156
923	a	43	580	220	a	157
924	a	44	584	224	a	158

925	a	45	594	234	a	159
926	a	46	595	235	a	160
927	a	47	615	256	a	161
928	a	48	616	257	a	162
929	a	49	624	265	a	163
930	a	50	626	267	a	164
931	a	51	628	269	a	165
932	a	52	632	273	a	166
933	a	53	634	275	a	167
934	a	54	637	279	a	168
935	a	55	641	283	a	169
936	a	56	644	287	a	170
937	a	57	645	288	a	171
938	a	58	646	289	a	172
939	a	59	648	291	a	173
940	a	60	652	296	a	174
941	a	61	662	307	a	175
942	a	62	671	316	a	176
943	a	63	672	317	a	177
944	a	64	675	320	a	178
945	a	65	677	322	a	179
946	a	66	684	331	a	180
947	a	67	685	332	a	181
948	a	68	686	333	a	182
949	a	69	693	343	a	183
950	a	70	703	356	a	184
951	a	71	704	357	a	185
952	a	72	709	363	a	186
953	a	73	710	364	a	187
954	a	74	711	366	a	188
955	a	75	715	371	a	189
956	a	76	723	380	a	190
957	a	77	724	381	a	191
958	a	78	731	388	a	192
959	a	79	734	391	a	193
960	a	80	745	406	a	194
961	a	81	753	415	a	195
962	a	82	754	416	a	196
963	a	83	758	420	a	197
964	a	84	760	422	a	198
965	a	85	764	426	a	199
966	a	86	765	427	a	200
967	a	87	766	428	a	201
968	a	88	774	437	a	202
969	a	89	776	439	a	203
970	a	90	778	441	a	204
971	a	91	785	448	a	205
972	a	92	788	452	a	206
973	a	93	793	457	a	207
974	a	94	795	459	a	208

975	a	95	797	461	a	209
976	a	96	806	471	a	210
977	a	97	812	477	a	211
978	a	98	820	486	a	212
979	a	99	823	489	a	213
980	a	100	827	493	a	214
981	a	101	833	499	a	215
982	a	102	834	500	a	216
983	a	103	842	509	a	217
984	a	104	852	521	a	218
985	a	105	854	523	a	219
986	a	106	858	529	a	220
987	a	107	863	536	a	221
988	a	108	864	539	a	222
989	a	109	865	540	a	223
990	a	110	867	542	a	224
991	a	111	872	548	a	225
992	a	112	877	553	a	226
993	a	113	878	554	a	227
994	a	114	880	556	a	228

a=sequences from USSN 08/561,469, filed November 17, 1995 (Attorney Docket No.:GTN-001CP).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

Other embodiments are within the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT
(A) NAME: Astra Aktiebolag
(B) STREET: S-151 85
(C) CITY: Sodertalje
(D) STATE:
(E) COUNTRY: Sweden
(F) POSTAL CODE (ZIP):

(ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS

(iii) NUMBER OF SEQUENCES: 268

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: CD/ROM ISO9660
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/561,469
(B) FILING DATE: 17-NOV-1995

(vii) CORRESPONDENCE ADDRESS:
(A) ADDRESEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, Suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: GTN-001CPPC

(x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617)227-7400
(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

```
ATGAAAGGYC CYATCCTATG GCCGGCGTTT TCTCAATTTA GCGATCAAGA TTTGAGCGAT      60
ATTGTGGCGT ATCTCACTTC TATTTTGCCT AAAAATTTGA GCGATAAGGA AGTGTTCGCG     120
CAAAGTTGTC AAAGGTGCCA TAGCCTGGAT TATGCTAAAG ATAAGGCCTT TAGCGATCCT     180
AAAGATTTAG CCAATTATTT AGGCTCTCAT GCGCCTGATT TGTCCATGAT GATTAGGGCT     240
AAGGGCGAAC ATGGCTTGAA TGTTTTCATC AACGATCCGC AAAAGCTTTT GCCTGGCACA     300
GCCATGCCTA GAGTGGGATT GAATGAAAAA GCTCAAAAAC AAGTCATTTC TTATTTGGAA     360
AAAGCGGGCG ATAGGAAAAA GCATGAAAGG AATACTTTAG GGATTAAGAT CATGATTTTC     420
TTTGCGGTGC TGTCGTTCTT GGCTTACGCT GGAAAAGAAA AGTTTGGAGC GAAGTGCATT     480
AAATTTAAAA AAGGGGGGAC ATGGTTTTAT GATTTTTAA                            519
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

```
ATGCAAGAAT TCAGTTTGTG GTGCGATTTT ATAGAAAGGG ATTTTTTAGA AAACGATTTT      60
TTAAAGCTCA TCAATAAGGG GGCTATTTGC GGGRCGACGA GTAACCCTAG TTTGTTTTGC     120
GAAGCGATCA CAAAAAGCGC GTTTTATCAA GATGAAATCG CTAAAMCTCA AAGGCAAAAA     180
AGCTAA                                                               186
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

```
TTGAASCCGA TGAAAGTGAT TCAAGTTTTT TTATTTTCCA ACCCTTTTTG CGCGATTGTG      60
CCTAACACGG AGCCAGAACA TTTGGAGCAT TATGACCACG ATTTAGAACC CTTTTTCTTC     120
GCTTATAAAT ATTTTTTAGA CCATGCTCAA AAAAGAGTGA TCTATAAAGA AGATCCTTTT     180
TTAAAAAACT ATTCTAAAGA CGCCATTGTT TTAGAAAAAA AAGACATTTA TAATATCCAA     240
TACATTTTAA AAGACGGAGA GCCTTACACT TCGTTTGAAT TGAAAAATTT GGGGGCTTTT     300
TTGGTGTGGG GGTTAGGCGA ACATAACGCC ACGAATGCGA GTTTGGCGAT TTTAAGCGCT     360
TTAGATGAAT TAAATTTAGA AGAAATTAGA AATAATTYAT TGAATTTTAA AGGCATTAAA     420
AAACGCTTTG ATATTTTGCA AAAAAACAAT CTCATTCTCA TTGATGATTA CGCCCACCAC     480
CCTACTGAAA TTGGCRCCAC TTTAAAAAGC GCTAGGATTT ATGCCAATTT ATTGAATACG     540
CAAGAAAAAA TTATAGTGAT CTGGCAAGCG CACAAATACT CTCGCTTAAT GGACAATTTA     600
GAAGAATTTA AAAAATGTTT TTTAGAGCAT TGCGACAGGT TGATCATTTT ACCCGTTTAT     660
AGCGCGAGTG AAGTTAAAAG AGACATTGAT TTGAAAGCCC ATTTTAAGCA TTATAACCCC     720
ACCTTTATAG ACAGGGTGCG TAAAAAGGGG GATTTTTTAG AGCTGTTAGT CAATGATAAT     780
GTGGTAGAAA CGATTGAAAA AGGCTTTGTG ATAGGCTTTG GAGCGGGGGA TATTACCTAT     840
CAGTTGAGAG GCGAAATGTA A                                               861
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

```
TTGTTGCTTT TCTTTCTTTT GAARGGCGTC GTTTTTTCTT TGGGCTTTTT TTCCTTTTTT      60
GAAGAAGTCT CTGGCTCTTT TGRAGCTGTT TCTTTGARCG TGTTAGCGTT AGTCATGGGG     120
TCTAGTYCTG GGTTAGAAGA ATTCTGTGTC TTAGAAGAGC TTATAAATTC AGGGCTATCA     180
GTATAG                                                               186
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

```
ATGGGTTTTT TAAAAGTTTT AAAACATGAC GCTTTAGGGC AAGTAGGGAA TATTGTTATA      60
GGGAATTTCT TAATAACGCT CACTGTTTTA GCGGTTTGTT TTTCCTCTCA AAGCGCTGAA     120
GAAACGACCA TGCTCACCCT AAGCTACACG CTCTTTTTTA TTTTAGGGGC GTTTTTATTA     180
GTCGCAATCA GCGTGGGAGC GATCAAAAAC CTCAACGCGC TTTTTTCTAA AAGAGGGCTT     240
TTAAGCTTTT CCTTACCCAT TAGTTTGGAA TCTTTATTGC TCCCTAAAAT CTTGCTCCCC     300
AKGGTGTTTT TTTATCTTCA GTTTGTTCTG GTTTGTGGCG AGCGTGCGTT TGGGCTATTA     360
CCTTTTTAA                                                             369
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

```
ATGTTAAAAA CCCACTTAAG CAGCGCTAGG GGCGTTGTGG TGTTGTCTAA GATTTTACCG      60
GTGAACGTGG TGTTAATGGT GAGCGTGCGC TTGTTTGAAA AGGAATTAAA ACGCAAACCT     120
TACTACATCA TTGCGAGCGC ACACAGCGAT GAAGGTTTAG AAAAATTAAA AAAATTWGGG     180
GYTGATATGG TGGKTTYCCC TACAAAACTY ATGGCGCAGA GAGTGAGCGC GAATKGMTGG     240
TGYKTCCTGG ATATGGAAAA TATCTTAGAG CGTTTTATCA ACAAAAAAGA CACGCTTTTA     300
GACTTAGAGG AAGTGATTGT CCCCAAAACC AGCTGGCTTG TGTTAAGGAA ATTAAAAGAA     360
GCCCATTTTA GAGAGATCGC TAAAGCCTTT GTGATTGGTA TCACTCAAAA AGATGGCAAA     420
TACATCCCCA TGCCTGACGG GGAAACGATT ATTGCAAGCG AATCCAAGCT ATTGATGGTT     480
GGCACTTCAG AAGGCGTTGC GACCTGTAAG CAACTCATTA CTAGCCACCA AAAACCAAAA     540
GAAGTGGATT ACATTTCATT GTGA                                             564
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

GTGGGGAGCT TTTTATTCGT GGGGCCTAGT GGGGTAGGGA AAACAGAATT GGCTAAAGAA 60
TTGGCCTTGA ATTTGMATTT GCATTTTGAA CGCTTTGACA TGAGCGAATA CAAAGAAGCC 120
CATAGCGTGG CAAAGCTCAT CGGAAGTCCT AGCGGTTATG TGGGGTTTGA GCAAGGGGGG 180
TTATTGGTGA ATGCGATTAA AAAGCACCCG CATTGTTTGC TGCTTTTAGA TGAGATAGAA 240
AAGGCCCACC CTAATGTGTA TGATTTGTTG TTGCAGGTGA TGGAKAACGC CACTTTGAGC 300
GATAATTTAG GCAACAAGGC GAGTTTTAAG CATGTGATAC TGATTATGAC KKCAARTGTG 360
GGGAGTAAGG ATAAGGACAC GCTAGGGTTT TTTAGCACTA AAAACGCCAA GTATGATAGA 420
GCCGTTAAAG AGCTTTTAAC CCCTGAATTC CGATCCAGAA TTCATGCCAT CGTCCCCTTT 480
AACGCGCTCA GTTTGGAGGA TTTTGAAACG CATTGTTTCT GTGGAATTGG ACGGGTTAAA 540
AGCCCTAGCA CTAGAGCAAG GCGTGATCTT AAAATTCCAT AA 582

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 909 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

ATGGCTTTTC AGGTCAATAC AAATATCAAT GCGATGAATG CGCATGTGCA ATCCGCACTC 60
ACTCAAAACG CACTTAAAAC TTCATTGGAG CGATTGAGTT CAGGTTTAAG GATCAATAAA 120
GCGGCTGATG ACGCATCAGG CATGACGGTG GCGGATTCTT TGCGTTCGCA AGCGAGCAGT 180
TTGGGTCAAG CGATTGCCAA CACGAATGAC GGCATGGGGA TTATCCAGGT TGCGGATAAG 240
GCTATGGATG AGCAATTAAA AATCTTAGAC ACCGTTAAGG TTAAAGCGAC TCAAGCGGCT 300
CAAGATGGGC AAACTACGGA ATCTCGTAAA GCGATTCAAT CTGACATCGT TCGTTTGATT 360
CAAGGTTTGG ATAATATCGG TAACACAACG ACTTATAACG GGCAAGCGTT ATTGTCTGGT 420
CAATTCACTA ACAAAGAATT CCAAGTAGGG GCTTATTCTA ACCAAAGCAT TAAGGCTTCT 480
ATCGGCTCTA CCACTTCCGA TAAAATCGGT CAGGTTCGTA TCGCTACAGG CGCGTTAATC 540
ACGGCTTCTG GGGATATTAG CTTGACTTTT AAACAAGTGG ATGGCGTGAA TGATGTAACT 600
TTAGAGAGCG TAAAAGTTTC TAGTTCAGCA GGCACAGGGA TCGGCGTGTT AGCAGAAGTG 660
ATCAATAAAA ACTCTAACCG AACAGGGGTT AAAGCTTATG CGAGCGTTAT CACCACGAGC 720
GATGTGGCGG TCCAGTCAGG AAGTTTGAGT AATTTAACCT TAAATGGGAT TCATTTGGGT 780
AATATCGCAG ATATTAAGMR AAACGACTCA GACGGAAGGT TAGTCACAGC RATCAATGCG 840
GTCACTTCAG AAACCGGTGT GGWAGCTTAT ACGGATCAAA AAGGACGCTT GAATTTGCGC 900
AGTATAGGT 909

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

```
ATGTTTTTTA AAACTTATCA AAAATTACTG GGCGCGAGCT GTTTGGCGCT GTATTTAGTG      60
GGCTGTGGGA ATGGTGGTGG CGGTGAATCG CCGGTTGAGA TGATTRCAAA TAGCGAGGGT     120
ACGTTTCAAA TCGACTCCAA AGCAGATAGC ATTACTATTC AAGCCCTCAA CCTTAATACA     180
GGTAATTGTG CTGTCAATTT TGTTCCAGTA AGTGAGACGT TTCAAATGGG TGTTTTAAGT     240
CAAGTTACTC CAATCTCTAT ACAGGATTTT AAAGATATGG CAAGCACTTA TAAGATATTT     300
GATCAAAAGA AAGGGTTGGC AAACATAGCA AATAAAATTT CTCAATTAGA GCAAAAGGGT     360
GTGATGATGA AACCTCMAAC CCTTAATTTT GGAGAAAGTT TAAAAGGCAT TTCTCAAGGG     420
TGCAATATTA TAGAGGCAGA AATACAAACC GACAAAGGCG CTTGGACTTT TAACTTTGAT     480
AAATAA                                                               486
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

```
GTGTGTTTAG GGCTAGCTGA TGTGATGGTG GTTTTAAGCT TGCACCTCAA CCTAAACCCC      60
ACCAACCCTA AATGGCTCAA TAGGGACAGG TTGGTTTTTA GCGGAGGGCA TGCGAGCGCG     120
TTAGTGTATA GTTTGTTGCA TTTGTGGGGC TTTGATTTGA GTTTAGACGA TTTAAAGCGT     180
TTCAGGCAAT TACACTCTAA AACCCCAGGA CACCCTGAAT TACACCACAC CGAAGGCATT     240
GAAATCACCA CASCCTTTAG GGCAAGGTTT TGCTAA                               276
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

```
ATGACAACAC CGATGATTAT TATTTCCCTA GAAATGGGGT TATCTTTAGT TCCTATGCGA      60
CAATGTCTGG TTTGCCAAGC TCTGGCACGC TCAATTTCTT GGAACGGGTT AGGCGGGAAT     120
GTCCGTAACA CCAAAGTTTA TGGTAAATTC GCCGCTTACC ACCATTTGCA AAAATATTTA     180
TTGATAGATT TGATCGCTCG TTTTAAAACG CAAGGGGGCT ATATCTTTAG GTATAACACC     240
GATGATTACT TGCCCTTAAA CTCCACTTTC TACATGGGGG GSGTAACCAC GGTGAGAGGC     300
TTTAGGAACG GCTCAATCAC ACCTAAAGAT GAGTTTGGCT TGTGGCTTGG AGGCGATGGG     360
ATTTTTACCR CTTCTACTGA ATTGAGCTAT GGGGTGTTAA AAGCGGCTAA AATGCGTTTA     420
GCGTGGTTTT TTGACTTTGG TTTCTTAACC TTTAAMACCC CAACTAGGGG GAGTTTCTTC     480
TATAACGCTY CCACCACGAC GGCGAATTTT AAAGATTATG RCGTTGTAGG GRCTGRGTTT     540
GARRGGGCGA CTTGGAGGGC T                                               561
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

```
ATGCAAGCGT TAAAATCATT GCTTGAAGTG ATTACAAAAC TCCAGAATCT AGGCGGCTAT      60
TTGATGCATA TAGCTATTTT CATCATTTTT ATTTGGATTG GAGGRCTTAA GTTTGTGCCT     120
TACGAAGCTG AAGGGATCGC CCCTTTTGTG RCCAACTCCC CTTTCTTTTC TTTCATGTAT     180
AAATTTGAAA AACCTGCATA CAAACAACAC AAAATGTCTG AATCCCAATC CATGCAAGAA     240
GAAATGCAAG ATAACCCTAA AATCGTTGAA AACAAAKAAT GGCATAAAGA AAACCGCACT     300
TCATTTAGTG GCTGA                                                      315
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

```
ATGCAGTTTG AAGAAATGAA AGAATTAGCC CATCAAATTG GCGTGTTTTA CCATGTTGGC      60
GTTGATGGCA TCGCGCTCTT TTTGTTGCTC TTAAACGCTA TCGTGGTGTT ATTGTCCGTG     120
GTTTATGTCA AAGAGCGTCG TAAAGACTTT GTGATTTGTC TTTTATTGTT AGAMGGGATC     180
TTAATGGGCG TGTTTTCTTC TCTTAATGTG ATCTTTTTCT ACGCTTTTTG GGAAATCTCG     240
CTCTTGCCGG TTTTATACCT CATCGGTCGT TTTGGCCGTA ATAACAAAAT CTATTCTGGC     300
ATGAAGTTTT TCCTCTACAC CTTTTTAGCG TCGTTGTGCA TGCTTTTAGG CATTTTATAC     360
ATCGGGTATG ACTACGCCAA TAATTACGGC ATGATGAGTT TTGATATTTT AGACTGGTAT     420
CAGTTGAATT TTTCTAGCGG GATTAAAACC TGGCTCTTTG TAGCTTTCTT AATAGGGATT     480
GCGGTTAAAA TCCCGCTCTT TCCCTTCACA CATGGCTGCC TTATGCGTAT TCTAACGCCC     540
CCACTCTAG                                                             549
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```
GTGAAAAAAT ACGCTGAAGA TTTTATCACC AAAGATGAAG TGAAATCCCT TTTAGAGCGC      60
TTGGCTAAAG ACTATCCTAC GATTGTAGAA GAGAGTAAAA AAATCCCCAC CGGTGCGATC     120
CGCTCAGTCT TGCAAGCCTT GTTGCATGAA AAAATCCCCA TTAAGGACAT GCTCACTATT     180
TTGGAAACGA TTACTGATAT TGCTCCATTG GTTCAAAACG ATGTGAATAT CTTAACCGAA     240
CAAGTGAGGG CGAGGCTTTC YAGGGTGATC ACCAACGCTT TTAAATCTGA AGACGGGCGT     300
TTGAAATTTT TAACCTTTTC TACCGATRGC GAACAATTTT TKGCTCAATA A               351
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```
ATGATGAAAA ACAAACGCTC TCAAAATAGC CCTTATGTAA CGCCTGACAA CCCTTATCTA      60
ACGCTAGAAA AAGCTTTAGG GTATTCTTTT AAAGACAAGC GTTTATTGGA GCAAGCCTTA     120
```

```
ACGCATAAAT CATGTAAGCT CGCTTTAAAC AATGAGCGCT TGGAATTTTT GGGCGATGCG     180
GTGTTGGGCT TGGTGATAGG GGAGCTGCTA TACCATAAAT TCTRTCAWTR CGATGGGGGC     240
AAACTCTCTA AATTAAGGGC TTCTATTGTG AGCGCGCATG GTTTCACTAA ATTAGCGAAA     300
GCGATTGCTT TACAAGATTA TTTGCGCGTT TCTTCTTCTG AAGAAATTTC TAAGGGGAGG     360
GAAAAACCCT CTATTCTRTC AAGCGCTTTT GAGGCTTTAA TGGCTGGGGT GTATTTAGAA     420
GCAGGGTTAG CTAAGGTGCG TAAAATCATA CAAAATTTAC TCAATCGTGC TTACAAGCGT     480
TTGGATTTGG AGCATTTGTT TATGGATTAT AAAACCGCTT TGCAGGAATT GACCCAAKCK     540
CAGTTTTGCG TGATCCCCAC TTACCAATTA CTCCAAGAAA AAGGCCCCGA TCACCATAAA     600
GAATTTGAAA TGGCTCTATA CATTCAAGAT AAAATGTATG CGACCGCTAA AGGCAAGAGT     660
AAAAAAGAAG CCGAACAGCA ATGCGCTTAT CAAGCGCTTC AAAACTTAAG GAAGCCAAAT     720
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

```
TTGCTGGTCT TACTCAATCT AAAGAWTACG CCGAATTTGA TGTGGCCTTT AGATATTATT      60
GTGGTTGTGG CATGGGTGTT ATGGGGGGTT AATATGTTTG GGAGCATGAG CGTTAGAAGA     120
GAGAATACTA TTTATGTGTC TTTGTGGTAT TACATCGCTA CTTATGTGGG TATAGCGGTG     180
ATGTATATCT TCAATAACCT TTCTATCCCC ACCTATTTTG TCGCTGATAT GGGGAGCGTT     240
TGGCATTMTA TTTCTATGTA TTCAGGCAGT AATGATGCGC TCATTCAATG GTGGTGGGGG     300
CATAATGCGG TCGCTTTTGT CTTTACGAGT GGGGTGATTG GCACAATTTA TTATTTCTTG     360
CCTAAAGAGA GCGGCCAGCC TATCTTTTCT TACAAACTCA CTTTGTTTTC TTTTTGGAGT     420
TTGATGTTTG TTTATATTTG GGCGGGCGGG CACCATTTGA TCTATTCCAC CGTGSCTGAT     480
KGRGTACAAA CCCTTTCTAG CGYGTTTTCA GTGGTGTTGA TCTTGCCTTC GYGGGGGACA     540
GCGATTAACA TGCTTTTAMC GATGAGAGGC CAATGGCACC AGYTCAAAGA AAGCCCTTTG     600
ATCAAGTTTT TAGTTTTAGC CTCAACTTTC TACATGCTTT CCACGCTAGA AGGCTCCATT     660
CAAGCCATTA AAAGCGTGAA CGCTTAG                                         687
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

```
ATGAAAGCAC CCTCCCAAYA GGATTTAAAA AAAATCTTAG GGATTGAAGA AGTCATAATS      60
STATCCACAA GCCCCATGGA ATTACGATTG GCCAATCAAA AGCTAGGCAA TCGTTTCATT     120
AAAACCTTAC AAGCCATGAA CGAATTAGAC ATGGGTGCAT TTTTTAACGC TTACGCTCAA     180
ACAACCAAAG ATCCCACCCA TGCCACTAGC TATGGCGTTT TTGCGGCGAG TTTGAATATG     240
GAATTGAAAA AGGCTTTAAG GCATTATCTT TATGCGCAAA CTTCTAACAT GGTGATCAAC     300
TGCGTTAAAA GCGTCCCCTT ATCCCAAAAC GACGGGCAAA AAATCTTATT GAGCTTGCAA     360
AGCCCTTTTA ACCAGCTCAT AGAAAAAACC CTAGAACTAG ACGAAAGCCA CTTGTGCGCA     420
GCAAGCGTTC AAAACGACAT TAAGGCGATG CAGCATGAGA GTTTATACTC GCGCCTTTAT     480
ATGTCTTGA                                                             489
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

```
ATGGCGTTTA TTCTAACCAC AAACCTATTT ATCAAGAGTT TTACGAACTC AATTCGCATA      60
ACGGGTTGTA TTATCAGCCC TAATGTGTTT TTTGCTTATG AATTTTGCGC GTTAGGGTTT     120
AGAAAAGGGG GGTTAATTTT GGATAATTTT TCTAAATTCG TGAGCCACAG GTTGCAATAA     180
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

```
GTGCGTTTTT TCATTTTTTT AATTCTCATT TGCCCTTTAA TATGCCCCTT AATGAGCGCG      60
GATAGCGCTT TACCTAGCGT CAATCTCTCT TTAAACGCTC CTAGTGATCC TAAACAACTC     120
GTAACCACCC TTAATGTCAT CGCCTTACTC ACGCTTTTGG TTTTAGCCCC ATCGTTGATT     180
TTAGTGATGA CGAGTTTCAC CCGTTTGATC GTGGTGTTTT CTTTTTTAAG GACCGCTTTA     240
GGCACGCAAC AAACCCCACC CACTCAAATT CTAGTCTCGC TCTCTTTGAT ATTGACTTTT     300
TTTATCATGG AACCTAGCTT GAAAAAGGCT TATGATACAG GGATTAAGCC TTATATGGAT     360
AAAAAGATTT CTTACACCGA AGCGTTTGAA AAAAGCACTC TGCCTTTCAA GGAATTCATG     420
CTTAAAAACA CACGAGAAAA AGATCTAGCC CTTTTTTTTA GGATTAGGAA TTTGCCTAAC     480
```

CCTAAAACCC CTGATGATGT GAGCTTGAGC GTTTTAATCC CGGCATTTAT GATAAGCGAG 540
TTGAAAACAG CGTTTCAAAT CGGCTTTTTA CTCTACTTGC CTTTTTTGGT GATTGATATG 600
GTTATCAGCT CTATTTTAAT GGCGATGGGT ATGATGATGC TCCCGCCTGT AATGATTTCT 660
CTGCCTTTTA AAATTTTGGT GTTTATTCTG GTGGATGGGT TTAATTTATT GACCGAAAAT 720
TTAGTGGCGA GTTTTAAAAT GGTTTAA 747

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

TTGTTGGTTA CTTTTTTGAA TGGGTTTGAC CCAAAAATCG CTAATTTAAG GAAAGCGTGC 60
AATGTTTATA GYGTGGGGGT GATTTATATT GTAACCACCA ACACGCTCAA TATTTTAAGT 120
TGTGAGAGTT TTGAAATTTT AGAAAAAAGA GAGCTGGATA CAAGCGGCGT TACTAAAACT 180
TCCACGCCGT TTTTTTCTAG GGTTGAGGGC ATTGATGCAG GCACGCTAGG GAAACTTTTT 240
TCAGGCAGTC AATCTAAAAA TTACTTCGCT TACTATGACG CTTTAGTGAA AAAAGAAAAA 300
CGAAAAGAAG TAAGGATTGA AAAGAAAGAA GAAAGGATTG ATGCTAGAGA AAATAAACGA 360
GAAATCAAGC AAGAAGCCAT TAAAGAGCCT AAAAAAGCCA ATCAAGGCAC AGAAAACGCT 420
CCCACTTTAG AAGAGAAAAS CTACCAAAAR GCAGAGCGAA AATTTGACGC TAAAGRAGRA 480
AGGMGATCGT TCAAGRGATG A 501

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ATGGAAAACA GCACACTTTA TATTGTTATT GCCGGCTTAT GGCTTGCTGT AGGCTTTGGA 60
ATCTTTTTAA AGAAATTAGA CATGCCCGTT ATCATTGGCT ACATTTGCAC AGGAACGGTC 120
TTAGCGGCTT TTTTTAAAAT TAATGATTTT AATTTGTTGT CTGATATTGG TGAATTTGGT 180
ATCGTCTTTT TAATGTTTAT GATAGGCATT GAGTTTAATT TTGACAAGCT CAAGTCCATC 240
AAACAAGAAG TGCTCGTTTT TGGGCTTTTA CAGGTTGTTT TATGCGCTTT AATCGCTTTT 300
TTATTGGGGT ATTTTGTTCT GGGTCTTTCG CCCATTTTTT CCCTTGTTTT AGGCATGGGG 360
CTTTCACTCT CTTCAACCGC C 381

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

TTGTTACTCA TGCTTAATAA GCCAAAGCCT TTATTTTTGM CTCTTGGTTA A 51

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

```
ATGGCATTAA GGGTATTATT ATTCTTTTGT TTTTTGTTTT TGCAAGCAGA AGATAAGAGC      60
CAAGAATTAT CATCTATACA AAAACAAATG GCTTTGGTGG ATAAAAAACT CGCCAAAGAC     120
GATAACGTGT GGTTGAAAAA ATTTGAAAAC TATAAAATTT ACAACCAAAT TTATACTGAA     180
AAAGAGAGCG TGAGGCAGGA ATTAAGGCGC TTAAAAAACA AAAAAAGCAA GGATTTATTA     240
AAGATTAGCA CCTTAGAGCA TACCTTAAAG GCTTTAGAGT CCCAGCAAAA AATGTTTGAA     300
AGCTATGGGG TCAATCCTTT TAAGGACTTG ATAGAGCGCC CCAATATCCC CAATATCCCT     360
AATATCGCTA ACCCTATTGC GATCATTGAT GGCATTTCTT TCATCAAGAG CATGCGTTTA     420
AAGCATGAAA ATCTTAAAAA TAACCAGACT TCTTTAGGAG AAGTTTTAAA GCTTTTAGAT     480
CAAAAACACC AGCTTTTAAA TCAGTGGCAC GCTTTGGATA AAAGCGCGAA ATTAAGCGAT     540
GAGATTTATC AAACTCAAGC CAAACGCTTA GAATTGCAAG GGGCTCAAAA CATTCTAAAA     600
ACCACRATCG GGATTTTCCA AAAAGACAGC GATGAAGCTA TAAGCATTGT CAAATCTCAA     660
GTTAAAAACC AGCTTTTTAA ATTGGTTTAT GTGTTTTTAG CGGCCCTTTT GAGCGTGGTG     720
TTTGCGTGGA TTTTAAAAAT CATTTCCAGT AAATACATTG AAAATAATGA GCGCGTCTAT     780
ACCGTGAATA AAGCCATTAA CTTCGTGAAT GTGAGCGTGA TCGKTKKAAT CTTKCTTTTT     840
TCTTATTTAG AAAACGTTAC TTACTTGGTA ACGGTTTTAG GCTTTGCGAG CGCGGGCTTA     900
GCGATTKCGA TGAAGGATTT ATTCATGAGC TTGCTCGGGT GGTTTATCAT TTTGATTGGG     960
GGGAGCGTGC ATGTGGGCGA TAGGGTGCGT ATCGCTAAGG GGACGGATAT TTTTATTGGC    1020
GATGTGTTGG ATACTTCTAA TGTTGTACAT TAA                                  1053
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ATGAAAGAAC AAGAATGGGA TTTAAGCGCT TTATTTGAAA ATAAAGAAAG CGCAGAAGAA 60
TTTTTAAAAA CCTTACAAAC AGAAGTGCAA GAATTTGAGA ACGCTTATCA AAATAACCTT 120
AAGAATTTAG ACGCTGCAAA ATTTGCCAAC ACTCTTAAAC ATTACGAAAA TTTGTCAGAA 180
AAGATCTCTA GAGCGATGGC TTACGCCAAT TACTTTTTGC CAAGAACACT AAAGAAGCGA 240
AGTTTTATTC GCAATGCAAA TGGCTTGTGC AAATATCCAA CAACACCTTT TATTCTTTGA 300

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

TTGCGCGTGG GCATGTATGA AGTGTGTAAC CATAAAGACG GCACCGCTTA TCATTCCACA 60
AGAGGTTCTA AGGTTACCTT AGCGTGTAAA ACCGGCACCG CGCAAGTCGT AGAAATCGCT 120
CAAAACATCG TCAATCGCAT GAAAGAAAAG GATATGGAAT ATTTCCATCS MTCCCATRCG 180
TGGATTACGR CATATCTTTR CCCTATGAAA AACCCAAATA CGCTATCACT ATTTTAG 237

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

```
TTGGGTTTGG TGWRCGGRAT TTCTCTCTTG CATTTGAGTT TGGAGCAAAA AATCAGCGTG      60
TTTCTTGGRC YCAATTTAAT GCTTTAYCCG GTCAYAGAGG TGCTTTTTAG TATCCTTAGG     120
CGCAAAATAA AACGCCAGAA AGCCACCCAT GCCGGATAA                             159
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

```
TTGGCTCAAC CGGTTCAGGT AAGAACAGTG TTTATGTCCA TGACTCTAAA CGCTATGGGG      60
CAATTTGCCT ATAATTTTCC TGCTAATATC AGCAAAGACA AGCAAAAGCT CACTATGGTT     120
TATATGGATA AAGATTATGG CGCTTATGGG AATATTGTTG CAATGGGTGG GGAGTATGTC     180
AAGATTGAGC TAGGGACAGA TACAGGATTA AATCCTTTTG CTTGGGCAGC TTGTGTGCAA     240
AAAACAAATG CAACAATGGA GCAAAAACAA ACAGCTATTT CTGTTGTCAA AGAGCTTGTG     300
AAAAACTTAG CAACTAAAAG CGATGAAAAA GATGAAAATG GCAACAGCAT CTCTTTTAGC     360
CTAGCAGATT CTAATACGCT TGCAGCGGCA GTAACCAACC TTATCACAGG AGATATGAAC     420
CTAGATTATC CTATCACTCA ACTTATTAAT GCTTTCGGGA AAGACCACAA TGATCCTAAT     480
GGGCTTGTCG CGCGATTAGC GCCTTTTTGC AAATCAACCA ATGGTGAATT TCAATGGCTT     540
TTTGACAATA AAGCAACAGA TCGCTTAGAT TTTTCAAAAA CGATTATTGG CGTTGATGGG     600
TCAAGTTTCT TAGACAATAA TGACGTTTCG CCTTTTATTT GTTTTTACCT TTTCGCTCGT     660
ATCCAAGAAG CAATGGATGG GCGTAGATTT GTCTTAGATA TTGATGAAGC GTGGAAATAT     720
TTAGGCGATC CAAAGGTCGC TTATTTTGTG AGAGACATGC TAAAAACTGC AAGGAAAAGA     780
AACGCTATTG TTAGACTTGC GACTCAAAGC ATCACTGATC TTTTGGCTTG CCCTATTGCT     840
GATACGATTA GAGAACAATG CCCTACAAAG ATTTTTTTGA GAAACGATGG GGGTAATCTT     900
TCTGATTACC AAAGATTAGC CAATGTTACA GAAAAAGAAT TTGAAATCAT CACTAAGGGG     960
CTGGATAGGA AAATCCTCTA CAAACAGGAT GGAAGCCCTA GCGTTATCGC TAGTTTTAAT    1020
TTGAGAGGCA TTCCTAAAGA ATATTTGAAA ATTTTATCCA CAGATACTGT ATTTGTCAAA    1080
GAAATTGACA AGATTATCCA AAACCATAGT ATCATAGATA AATATCAGCC TTGA           1134
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ATGAAATTGG TGAGTCTTAT TGTAGCGTTA GTTTTTTGTT GTTTTTTAGG GGCTGTAGAG 60
TTGCCTGGAG TTTATCAAAC TCAAGAATTT TTATACATGA AAAGCTCTTT TGTGGAGTTT 120
TTTGAGCATA ACGGGAAGTT CTATGCCTAT GGTATTTCTG ATGTGRATGR CTCTAAAGCC 180
AAAAAAGACA AACTCAATCC TAACCCAAAG CTAAGGAATC GCAGCGATAA AGGCGTGGTG 240
TTTTTAAGCG ATTTGATTAA GGTTGGGGAA CAATCTTATA AAGGCGGTAA GGCGTRTAAT 300
TTTTRTGACG GCAAGACCTM CCATGTGAGA GTCACTCAAA RTTCAAACGG GGATTTGRAA 360
TTCACTTCAA GCTATGRCAA ATGGGGGTAT GTGGGCAAAA CCTTCACCTG GAAACGCCTG 420
AGCGATGAAG AAATCAAAAA TCTAAAGCTC AAGCGTTTTA ACTGA 465

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

TTGGAGACCC TATTCTTGGT ATAG 24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

ATGSACACAC ACGACAGGCG CAAGTTAAGA ATTARCCTTA CACAAACGAC GACTTTAGTG 60

GCCACTATTG GCTCAAACGC CCCTTATATC GGTCTTTTAG GGACGGTTAT GGGGATCATG 120
CTCACCTTTA TGGATTTAGG CTCAGCTTCT GGCATTGACA CTAAGGCGAT CATGACTAAT 180
TTAGCCCTTG CTTTAAAAGC GACCGGCATG GGGTTATTGG TAGCGATCCC TGCGATTGTG 240
ATTTATAACT TGTTAGTGAG AAAAAGCGAG ATTTTAGTTA CCAAATGGGA TATTTTCCAC 300
CATCCGGTTG ATACGCAATC CCATGAGGTT TATAGCAAAG CCTAA 345

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

ATGCAGGATT TAGACAATAA CATGTCCTTA GACACCGCTC ACAACACGCT GAGTTCTAAC 60
GGGAAAAACA TCACCATTGC CGGGGTGGTA AAAGCCTTAC AAAAAATTGG CGTGAGCGCT 120
AAGGGGATGG TTTCAATCTT GCAAGCCCTA AAAAAAAGCG GCGCGATTAG CGCGAAATGG 180
AGATACTATG ATAAACAACA ATAA 204

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

TTGCACCCTT TAGCGGATGT CTTTGTGGTG AATGACAAAC GGYCCGTTTT AGCGATGGTA 60
RCGATGTTGA TTGRCTCGTT AGCGAATATC TTTTTCAATT ACTTGTTTAT TTTTGKGTTG 120
GAAGTGGGGG TTCAAGGCAG MGCGATAGTC ACCGTGATAG GGCATGCGAT AGGGGGTTTA 180
GTCTTAATGC AGCATTTTTG GCGCAAAAAA GGGGAGTTGT ATTTTATCAA ACTGATTTTC 240
TTTATCTTCA GTCATTTCTT CAGCTAA 267

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

```
ATGTTAAGGA AAAACATTTT AGCTTACTAT GGGGCGAATT TTCTCTTAAT CATCGCTCAA     60
AGCTTGCCCC ATGCGATTTT AACCCCCTTG TTGCTTTCTA AAGGGCTTAG TTTGAGTGAA    120
ATCTTGCTCG TGCAAACCTT TTTTAGTTTT TGCGTGCTGG TGGCTGAATA CCCAAGCGGC    180
GTTTTAGCGG ATTTGATGAG CCGGAAGAAT TTATTCCTGG TTTCTAATGT GTTTTTAATC    240
GCTAGTTTTT CGTTGGTGCT GTTTTTTGAT AGTTTTATCC TCATGCTTTT AGCGTGGGGG    300
TTGTATGGTT TGTATAGCGC ATGCTCTAGC GGCACGATTG AAGCTTCACT CATCACAGAC    360
ATTAAGGAAA ACAAAAAAGA TTTATCCAAG TTTTTAGCCA AAAACAATCA AATTACTTAT    420
TTGGGCATGA TTATAGGGAG TTCTTTGGGA TCGTTTTTGT ATCTCAAAGT CCATGCGATG    480
CTGTATGTCG TGGGGATTTT TTTAATCATG CTCTGTGCGC TAACAATCAT CATTTATTTT    540
AAAGAAAAAG AAGGGGATTT TAAAAGCCAA AAAAATTTGA AACTCCTTAA AGAGCAAGTC    600
AAAGGCAGTC TTAAAGAGCT TAAAGATAAC CCCAAGCTTA AAATTTTGTT AGTGGGGCAT    660
TTGATTACGC CTGTCTTTTT TATGAGCCAT TTCCAAATGT GGCAAGCGTA TTTTTTAAAA    720
CAAGGCGTTA AAGAGCAATA CCTTTTTGTG TTCTATATCG CTTTTCAAGT GATTTCCATC    780
CCTCATTCAT TTTTTAAAAG CCAAAAATTA KCAGCCAAAA AATCGCCCTG A             831
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

```
TTGTATCCGC CGGGATCTGT GGTTAAAATG GGCGTGGGGT TAAGCTTTTT AGAAAACCTT     60
CATATCACAG AAAACACCAC TATCCCCACA CCGCCTTTTA TTGAAGTGGG CAAGCGCAAA    120
TTCAGGGACT GGAAAAAAAC AGGGCATGGC AATTCTAATT TGTATAAAGC CATTAGGGAG    180
TCCGTGGATG TGTATTTTTA TAAGTTTGGG CTTGAAATCT CTATAGAAAA MCTCTCTAAA    240
MCCTTTAAGG RAAGTGGRCT TTGGGGAAAA AACGGRCGTT GA                       282
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

```
ATGGCACACC ATKAAGAACA ACACGGCGGG CACCACCACC AYCACCACCA CACACACCAC      60
CACCATTATC ATGGCGGCGA ACACCACCAT CACCACCACA GYTCTCATCA TGAAGAAGGT     120
TGTTGCAGCA CTAGCGATAG TCATCATCAA GAAGAAGGTT GTTGYCACGG GYAYCACGAG     180
TAA                                                                   183
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

```
TTGGTTAAAA TAAGGTTATT TGATTTTACT ATAAGGTTGT TTAAACCTGA ATTTCACATT      60
TTTGATTTTT TAAAAGGGAT TAGAGTTCTT ATGATTGAAT GGATGCAAAA TCATAGAAAG     120
TATTTAGTGG TTACGATATG GATAAGCACG ATCGCTTTTA TTGCCGCCGG AATGATAGGT     180
TGGGGGCAAT ACAGCTTTTC TTTAGATAGC GATAGCGCTG CCAAAGTGGG ACAGATTAAG     240
ATTTCTCAAG AAGAATTAGC CCAAGAATAC CGCCGCCTTA AAGACGCCTA TGCTGAGTCT     300
ATCCCTGATT TTAAAGAACT CACCGAAGAT CAAATCAAAG CCATGCATTT AGAAAAAAGC     360
GCGCTAGATT CGCTCATCAA TCAAGCTTTA TTGAGGAATT TCGCTTTAGA TTTAGGGCTT     420
GGTGCTACCA AGCAAGAAGT GGCCAAAGAG ATCAGAAAAA CGAACGTTTT TCAAAAAGAT     480
GGCGTTTTTG ATGAAGAATT GTATAAAAAT ATCTTAAAAC AAAGCCATTA CCGCCCCAAG     540
CATTTTGAAG AAAGCGTTGA AAGGCTTTTA ATCCTTCAAA AAATCAGCGC TCTATTCCCC     600
AAAACCACCA CCCCTTTGGA GCAATCCAGT CTATCGCTTT GGGCAAAATT GCAAGACAAA     660
TTAGACATTC TTATCCTAAA TCCTAATGAT GTTAAAATCT CTCTCAATGA AGAAGAGATG     720
AAAAAATATT ATGAAAACCA TAGAAAGGAT TTTAAAAAGC CCACAAGCTT TAAAACACGC     780
TCTTTATATT TTGACGCTAG TTTAGAAAAA ACTGATTTGA AAGAGTTGGA GGAATACTAC     840
CATAAAAACA AGGTGTCTTA TTTGGACAAM AGMGGGGAAA TTACAGGATT TTAA           894
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

ATGGTTAAAC ACTATCTTTT CATGGCGGTT TCGCAGGTCT TTTTCTCCTT CTTTTTAGTG 60
CTGTTTTTTA TCTCTTCCAT TGTGTTATTA ATCAGTATTG CAAGCGTAAC GCTCGTGATT 120
AAAGTGAGCT TTTTGGATCT GGTGCAACTC TTTTTGTATT CCTTGCCWGG AACCATTTTT 180
TTTATTTTGC CGATYACTTT TTTTGCGGCT TKGCGYTTGG GGSTTTCAAG GCTTAGCTAT 240
GACCATGAAT TGTTAGTGTT TTTTCTCYTT TAG 273

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

ATGAGTAAAA GAGCGATCCG TTTCCCTAAC AAGCTTTTTT CATACCCTAA ACCCAAAATA 60
AAAGCGACAA ACACAAGCCA CACCGTTTTA TTCGCATACC CGCTCAAACC CCACGAAATG 120
GCCTTATTAG CGCTCGCTAC CTCACTGCTC GCTCCAATTT TTAACGCTAT ACACAGCACT 180
AACGCGCTCA ACGCTATCAA ACCTGATGGC ACCGGCTCTA AAATTAACCC TATAATCATG 240
CCCATGAAAA TACAAAAATA A 261

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

```
GTGTATAGCC GTTTTTTTGC CAACCAGCAT GAATTTGACT TTGAAGCTCA AGGGGCGCTA      60
GGGAGCGATC AATCAAGCTT GAATTTCAAA AGTACTCTAT TACAAGATTT GAATCAAAGC     120
TATAATTACT TAGCCTATAG CGCCACAGCA AGAGCGAGTT ATGGTTATGA CTTCGCGTTT     180
TTTAGGAACG CTTTAGTGTT AAAACCAAGC GTGGGCGTGA GCTATAACCA TTTAGGTTCA     240
ACCAACTTTA AAAGCAATAG CCAATCACAA GTGGCTTTAA AAAATGGCGC GAGCAGTCAG     300
CATTTATTCA ACGCTAACGC AACGTGGAAG CGCGTTATTA TTATGGGGAC ACTTCATACT     360
TTTATTTGCA TGTGGGAGTT TTACAAGAGT TCGCTCACTT TGGATCGAAT GATGTGGCGT     420
CTTTAA                                                               426
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

```
ATGYATGAAA ATGGTAGGGG TGTACCTAAA GATTACAAGA AAGCGGTTGA ATATTTCCAA      60
AAAGCTGTTG ATAACGATAT ACCTAGAGGG TATAACAATT TGGGCGTGAT GTATAAAGAG     120
GGTAAGGGAG TTCCTAAAGA TGAAAAGAAA GCGGTGGAAT ATTTTAGAAT AGCTACAGAG     180
AAAGGTTATA CTAACGCTTA TATCAACTTA GGCATCATGT ATATGGAGGG CAGGGGAGTT     240
CCAAGTAACT ATGCGAAAGC GACAGAATGT TTTAGAAAAG CGATGCATAA GGGCAATGTG     300
RAAGCTTATA TTCTCCTAGG GGATATTTAT TATAGCGGAA TGATCAATTG GGTATTGAGC     360
CGGACAAAGA TAAGGCTGGT CCATTATAAA ATGGCGGCCG ATGTRAGTTC TTCYAGAGCY     420
TATRAAGGGT TGTCAGAGTC YTATCSGTAT GGGYTAGGCG TGGAAAAAGA KWAAAAAAAG     480
GCYGAAGAAT ACATGCAAAA AGCATGCGAT TTTGACATTG ATAAAAATTG TAAGAAAAAG     540
AACACTTCAA GCCGATAA                                                  558
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

```
TTGCTCAACA TGTGGGATGA AGCCAAGAAA GAAGGGATCA ACATCAATAC AGAAAAGCTC      60
```

```
TCTCAAGAAT TGGGGGTTGT GTGCGTGCCA ACAAGCGCGA GATYCAAAGA AGATCGCTTG     120
AACACAGAGC TTTTATTAGA CGAAATTGTC AGGCTTTATT CTCAAAACAC TACAAACAAC     180
GAAAACATCA AAGTCCCATC TCAAAGTTTT AAAGAGTCTT TAAAATACAG CCAGAGCGCC     240
CAAAGAATCG CTAAATCAGT GATCAGTGAA AACAAACAAA ATGCGAGTTT TGAACACACT     300
TATAAGATTG ATAAGATTTT TAATGCACCA GCGTTATGGG ATTTTCATTT TTTTDGGGTT     360
TATGTTTATC ATCTTTTCTT TGAGCTTTTT AATAGGAGGG GGAGTGCRAA AAGCCCTTGA     420
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```
ATGCAAGAAG CGTTGTTGCG TTTTCAAGAG GGCTTTAAGG AGTGGGGTTA TCTTATTTTA      60
TTTTTGTATT CTTTGGGGGG TGGGTATGTA GGGATTGTCA TCGCTTCCAT TTTGAGCGCT     120
ACCACGCACG CTTTGGATAT AAAAATAACC ATTCTTGTCG CTTTTTTAGG GAATTTAATA     180
GGGAGTGGGG CTCTTGTAAT CTTTGCCCGC TATCAAAAAA GAGAGTTTTT AAAGTATTTC     240
CAAAAGCATA GAAGAAAGCT TGCTTTGGCG AGTTTGTGGG TGAAACGCTA CGCCTTGCTC     300
ATGATTTTTG TCAATAAATA TCTCTATGGG ATTAAAAGCG TTGTGCCTTT GGCAATTGGT     360
TTTAGCAAAT ACCCTTTAAA AAAGTTTTTA TGGCTTAATG TTTTTTCCAG TTTTTTGTGG     420
GCGTTAATCG TGGGGAGCGT TTCTTTTCAA GCGAGCGATT GGGTGAAAAC GCTGTATGAA     480
AGGCTTTCTC ATTACACTTC GTTTTTTGTC ATAAGTTTTG TTCTTATAGC GCTTTTAATA     540
TGGTTTTTAT TGAAACGATA TTCGCGCAAA ATGGGKTTTT AA                        582
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

```
ATGCGAAAGG GGCGTGTGAT GTTATGCGTG TTTGATATAG AAACCATTCC TAATATAAGC      60
TTGTGTAAAG AGCATTTTCA ATTAAAAGAA GACGATGCGC TAAAAATCTG TGAATGGAGT     120
TTTGAAAAGC AAAAAGAAAA AAGCGGGAGC GAGTTTTTGC CCCTTTATTT GCATGAAATC     180
ATCTCTATTG CAGCMGTCAT TGGCGATGAT TACGGGCAAT TTATCAAAGT AGGGAATTTT     240
GGTCAAAAAC ACGAGAATAA AGAGGATTTT GCGAGCGAAA AAGAGCTTTT AGAGGACTTT     300
```

TTCAAATACT TTAACGAAAA GCAACCGCGC CTAATAAGCT TTAAWGGCAG GGGTTTTGGA 360
TATTCCCCTA CTCACGCTCA AAGCCCTTAA 390

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

ATGGCTAAAA AGAAAATTGC GATCAGCTGT GGGGATATTC AAGGCGTAGG CTTAGAATTG 60
ATCTTAAAAA GCCATAAGGA AGTGAGTGCA CTTTGTGAGC CGTTGTATCT CGTTCATAGC 120
GAACTTCTAG AACGAGCCAA TCAATTGCTT GATAACGCTT ATGAAACTAA AACGCTTAAT 180
GCGATCGCTA TTGATGCCCC TTTACCCTTA TTAAACTCTA GCACGATAGG CAAAGTCAGC 240
ACTCAAAGCG GGGCGTATAG CTTTGAGAGT TTTAAAAAGG CTTGCGAGTT GGCGGATAGT 300
AAAGAAGTGG ATGGCATTTG CACTTTGCCT ATCAACAAAC TCGCATGGCA ACAAGCTCAA 360
ATCCCTTTTG TGGGGCATAC CGATTTTTTG AAACAACGCT ACAAAGATCA TCAAATTATT 420
ATGATGCTTG GGTGTTCAAA ACTCTTTGTG GGGCTATTTA GCGACCATGT GCCTTTAAGC 480
GCGGTTTCTC AACTCATTCA AGTGAAAGCG TTAGTTAAGT TTTTATTAGC GTTTCAAAAA 540
AGCACTCAAG CCAAAATCGT TCAAGTGTGT GGTTTCAACC CCCATGCGGG CGAAGAGGGA 600
TTGTTTGGGG AAGAAGATGA AAAGATTTTA AAAGCCATTC AAGAGAGCAA CCAAACGCTA 660
GGTTTTGAAT GCTTTTTGGG GCCACTGCCC GCTGATAGCG CTTTTGCCCC CAATAAACGC 720
AAAATAACCC CCTTTTATGT GAGCATGAGC CATGATGTAG GGCTAGCCCC TTTAAAAGCG 780
CTCTATTTTG ATGAAAGCAT CAATGTGAGT TTGAACGCTC CCATTTTACG CGCTTCCACT 840
GACCACGGCA CGGCGTTTGA TATTGCTTAT CAAAATAAGG CGAACCATAA AAGCTATTTG 900
AACGCGATCA AATACTTGGC TTAA 924

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

ATGAGCAGCG GGTTAATTTA CATTTCRTTA GAAGTCTTGG TARCGTGTTT GATCACCGCT 60
CTAATCATGT ATTATGTGAT GAAAAAGATC TATTACGCTA GAGGGCAAGC CATTTTAAAA 120
GGCGCTTCAG CCAAAGCTAA ATTAATGGAA TTTCAAGCGA AATCTTTCGT GGAAGCTGAA 180

GAAATGCGCA TGAAAAGCCA AGAATGCAAG TTGCAACAGC AATATGAAAA TAAGAATTTG 240
CAACTCCAAA CCCATTTTGA TAAAAAAGAA GCGCATTTGA AGCATTTAGA AGCGCAGCAC 300
AAAGAATTTG TAAGAGATGA AAAACGCTAT TTGGAAAAGG AAAAAAAAGA GCTTGAAAAA 360
GAACGCCAAA TTTTAGAAMM AGAGAGGGAA AATTTTRRRR RSCAGCGCGC CTTTGTRRRG 420
RRGSCTCRRG CCAAAGCGCT 440

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

ATGAATATCA AAATTTTAAA AATATTAGTT GGAGGGTTAT TTTTTTTGAG CTTGAACGCC 60
CATTTATGGG GGAAACAAGA CAATAGCTTT TTAGGGATTG GTGAAAGAGC CTATAAAAGC 120
GGGAATTATT CTAAAGCGGC GTCTTATTTT AAAAAAGCAT GCAACGATGG GGTGAGTGAA 180
GGCTGCACGC AATTAGGAAT CATTTATGAA AACGGGCAAG GCACTAGAAT AGATTATAAA 240
AAAGCCCTAG AATATTATAA AACCGCATGC CAGGCTGATG ATAGGGAAGG GTGTTTTGGC 300
TTAGGGGGGC TTTATGATGA GGGTTTAGGC ACGGCTCAAA ATTATCAAGA AGCCMTTGAC 360
GCTTACGCAA GGCATGCGTT TTAA 384

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

ATGGCGATAG CCATTAAGGA TTTATTGAGC GCTTATAAAG TCGTTTTACC TTTGGATAAA 60
ATCAGCATGC CATCTAGCGC GGATTTGAAG CTCACTTTGC AATTCTTAAA AAACACCGCC 120
CCCTTATTTA GCGTTCAAGG CAGCGTTAAT TTGCAAGAAG GCACTTTCTC GCTCTATAAT 180
ATCCCCCTTT ACACGCAAAG CGCTCAAATC AATTTGGACA TCGCCCAAGA ATACCAATAC 240
ATCTACATAG ACACGATCCA CACGCGCTAT GCAAACATGC KGGATTTAGA CGCTAAAATC 300
GCTTTAGATT TAGGTCAAAA AAACCTYTCY YKGGAKKCYY TAGGKCCATA A 351

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

```
ATGCCGGATA AYTTGCATTT GCACACCCTT TTATYTAAAT TCTTGCAACA ACGCTCTTTC      60
AATTACCCTA ACCCTTTATG CGCGTTTATC CTTATTCTAT GCAACCTGCC TTTTATTTTA     120
ATAAGCGTTT TGTTTCGCTT GGACGCTTAT GCGCTCATTG TGATTAGCCT AGTCTTTATC     180
RCATGCTATT TAATAGGCTM TGCTTATTTG AATAGGCAAG TTTGCGCTTT AGAAAAGCGG     240
GCGTTTTAA                                                             249
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

```
TTGAAAGTAA CRAATCCGCA TTTGTTGGTG GTAATCCAAG ATTTAAACGC TCGCATCGCT      60
TTAATGAAAC TCTTATTCCA AAACGTTAAG AGCGCGAACA AAGAATTGGT TTTTTGCAAT     120
AAAGAAAAAC GCTTGATAAG GTCTTTTGAT GCACAAAAAG AATACGGCAT CACGCCTGTA     180
GAAAATATTT TAAGCGTTTT AGACACCGCT ATGAATCCTA ACAGCGCGCT TGTGATAGAC     240
AATCTCAACG AAGCGAAAGA ATTGCACGAC AAAGTAGGGG CGGAAAAGTT AAAATCGTTT     300
TTAGAAAAAG CCCMTAGACA ACGAGCAGTA TTGCGTCATT TTTGCGCATG A               351
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

```
ATGAAAGAAT CTTTTTACAT AGAGGGAATG ACTTGCACGG CGTGTTCTAG CGGGATTGAA      60
CGCTCTTTAG GACGTAAAAG TTTTGTGAAA AAAATAGAAG TGAGCCTTTT AAATAAGAGC     120
GCTAACATTG AATTTAACGA AAATGAAACC AATTTAGACG AAATTTTTAA ACTCATTGAA     180
AAACTGGGTT ATAGCCCTAA AAAAACTCTA GCAGAAGAAA AAAAAGAATT TTTTAGCCCT     240
AATGTTAAAT TAGCGTTGGC GGTTATTTTC ACGCTTTTTG TGGTGTATCT TTCTATGGGG     300
GCGATGCTTA GCCCTAGCCT TTTACCTGAA AGCTTGCTTA CGATTAACCA TCATAGTAAT     360
TTTTTAAACG CTTGCTTACA GCTTATAGGC GCGCTCATTG TCATGCATTT GGGGAGGGAT     420
TTTTACATTC AAGGGTTTAA AGCCTTATGG CACAGACAAC CCAACATGAG CAGCCTTATC     480
GCCATAGGCA CAAGTGCTGC CTTAATTTCA GCCTGTGGCA ATTGTATTTG GTTTATACCA     540
ATCATTATAC CGATCAGTGG TCTTATGGGC ATTATTATTT TGAAAGCGTG TGCGTGA        597
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

```
GTGGGGATTG TGCCGGATAA TTTGTGGAAG CTCAAACGCT TCAATCAAGA CTGGCGCGTT      60
GGGGACACGC TCATTACTGC TATTGGGCAA GGCTCTTTTT TAGCCACGCC TTTGCAGGTG     120
TTAGCCTACA CAGGACTCAT TGCGACAGGC AAACTGGCAA CGCCTCATTT TGCTATCCAT     180
AACCAACAAC CGCTCAAAGA CCCCCTGAAT AGGTTTTCAA AAAAAGAAGC TCCAAGCCTT     240
GCGCGTGGGC ATGTATGA                                                  258
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1032 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

```
ATGCAAAACT TATTGATACA AGCAGAAAAT GCAATCGCTC TACTTTTTTT GTTAAATGAC      60
AAAAACCTAA AAGGAAAAAT AGATTTGATA TATATTGACC CTCCATTTGC TACAAACAAT     120
CATTTTACTA TCACAAATGG TAGAGCAACC ACAATTAGCA ATTCTAAGAA TGGCGATATT     180
GCTTATAGTG ATAAAGTAGT GGGTATGGAT TTTATGGAAT TTTTAAAACA ACGCCTGGTA     240
TTGCTTAAAG AATTGCTTTC AGAACAAGGC TCTATCTATG TGCATACAGA TTACAAGATA     300
GGGCATTATG TCAAGGTAAT GTTAGATGAA ATATTTGGCA TACAAAATTT TAGAAATGAA     360
ATCACACGCA TAAAGTGCAA TCCTAAAAAT TTTAAAAGGA TAGGCTATGG TAACATAAAA     420
GATATGATTT TATTTTACTC TAAAGGAAAA AATCCCATTT TTAACGAACC TAAGATCCCT     480
TATACGCCAC AAGATTTAGA AAAACGATTC CCTAAAATTG ACAAAGATAA AAGGCGTTAC     540
ACTACCGTTC CAATACATGC TCCAGGAGAA GTGGAAAGTG GCGAATGTTC TAAAGCATTT     600
AAAGGTATGC TACCTCCAAA AGGGCGGCAT TGGCGCACTG ATATTGCCAC ACTTGAGCGT     660
TGGGATAAAG AAGGTTTGAT TGAGTATTCT AACAATAATA ACCCTAGAAA AAAAATTTAT     720
GCCTTAGAAC AAGTTGGCAA AAGAGTCCAA GACATCTCGC AATTTAAACA CCCACAATAT     780
CCAAGCTACC CTACAGAAAA AAACGCTCAA TTATTAGACT TAATCATTAA AACCTCTTCT     840
AATAAAGATA GTATTGTTTT AGATTGTTTT TGTGGTTCTG GAACAACCTT AAAATCTGCG     900
TTTTTATTGC AACGAAAATT TATAGGCATT GATAATTCCG ATTTGGCTAT CCAAGCTTGC     960
AAAAACAAGC TTGAAACAAT AACAAAAGAC TTGTTTGTTT CTCAAAATTT TTATGATTTC    1020
CTTGTTTTTT AA                                                        1032
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

```
ATGACAAGCG TTGTCATCAA GCCCCATGCC TATGGCGAGC AAGTCCAAGA AATAGAAGAA      60
GAGTCAGATA GCGATTATGA AAAGAATAAC GACCAGGAAG CGATCAATTT TGGTATCGCC     120
TTGCATAAGG GATTGGAATA CCAATACGCT TACAACATTC CTAAACAAAG CGTTTTAGAA     180
TATTTAAACT ACCACTATGG TTTTTATGGT TTGGATTACC AAGCGTTAGA AGAAAGTTTA     240
GAGCTTTTTG AAAACGATGC AGGGATACAA GCCCTTTTTA AAAATCATGC CTTAAAGGGT     300
GAAGCGGCTT TTTTATTCCA AGGGGTTGTG TCTAGGATTG ATGTTTTATT GTGGGATAGA     360
GGGCAAAATT TGTATGTTTT AGATTATAAA AGCTCTCAAA ATTACCAGCA AAGCCATAAA     420
GCGCAAGTGT CTCATTACGC TGAGTTTTTG CGAACTCAAG SCCCCCATTT TAAGATACAA     480
GCGGGCATTA TTTACGCTCA TAAAAGACTG CTTGAAAAAT YATGGGKTTG A              531
```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

ATGTCTGAGG ATTTGCCTTT TGCGAGCGAT TCGCAATTCA CTTACAATGG GGTGAGCATC 60
ACGCGCCCCA CTAATGAGGT CAATGATGTG ATCAGCGGGG TTAATATCAC TTTAGAGCAA 120
ACCACAGAGC CTAATAAGCC TGCCATTATC AGCGTGAGCA GAGACAATCA AGCCATTATA 180
GACAGCCTTA AAGAATTTGT CAAAGCCTAT AATGAGCTTA TCCCTAAACT AGACGAAGAC 240
ACGCGCTATG ACGCTGACAC TAAAATCGCC GGGATTTTTA ACGGCGTGGG CGATATTCGT 300
GCCATTAGAT CCTCTCTTAA TAATGTGTTT TCTTATAGCG TGCATACGGA TAATGGGGTA 360
GAAAGCTTGA TGAAATACGG GCTTAGTTTA GACGATAAGG GCGTGATGAG TTTGGATGAA 420
GCTAAATTAT CAAGTGCATT AAATTCTAAC CCTAAAGCGA CTCAAGATTT TTTCTATGGG 480
AGCGATAGCA AGGATATGGG GGGCAGAGAA ATCCACCAAG AGGGCATTTT TTCTAAATTC 540
AATCAAGTCA TCGCTAACCT CATAGATGGA GGGAACGCTA AATTAAAGAT TTATGAAGAT 600
TCCCTAGACA GAGACGCTAA AAGCCTGACC AAAGACAAAG AAAACGCTCA AGAGCTTTTA 660
AAAACCCGCT ATAACATCAT GGCGGAGCGC TTTGCCGCTT ATGATAGTCA AATCTCTAAA 720
GCCAATCAAA AATTCAATTC CGTGCAAATG ATGATCGATC AAGCAGCGGC TAAAAAGAAT 780
TAA 783

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

ATGCGCATCG TATTTATGGG AACGCCTAGT TTTGCTGAAG TGATCTTAAG GGCGTTGGTT 60
GAAAATGAAG ATAAAAAGAT AGAAGTGGTG GGGCTATTCA CTCAAAGGGA CAAACCTTTT 120
GGGCGCAAAA AAGAATTGAA AGCCCCAGAG ACTAAAACAT ACATTTTAGA AAATCATTTA 180
AATATTCCCA TTTTCCAGCC GCAAAGTTTG AAAGAGCCTG AAGTTCAAAT CTTAAAAGGT 240
TTGAAGCCTG ATTTTATCGT GGTGGTGGCT TATGGTAAGA TTTTGCCTAA AGAGGTTTTA 300
ACCATCGCTC CTTGCATTAA TTTGCATGCG TCGTTATTGC CCAAATACAG GGGGGCTTCG 360
CCCATTCATG AGATGATACT CAATGACGAT AGGATTTATG GCATAAGCAC CATGCTTATG 420
GAKTTTGGAA TTGGATAG 438

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

```
ATGCGTTTTT ATTTTAAATT CCTTTGGCTT TTAGGGATTT TTCTTATTTT TTATTTTTTA      60
GACATTAAAG GCAGCTCTTC TTATATCAGC GACCGGGTTA AAAGCGCCTT GATGAGCGCG     120
AAAAACAGCT TACTAGACAA CGTTCAAGCG TATTTTTTTC AAGCCCAAAA CATTAAGGAA     180
TTTCAAAAAG AACGCTTGAT TTTAGAAGCT TTAAAACTAG AAAACGCTGA TTTGAAAGAG     240
CGTTTGAATA GTATTTATCC TTTAGAAAAT CCAAAAATGA CTTATACCCC TACTTTCATG     300
ACTTCATTCA TCAATTTAGA AGACACACAC AGCGTTTCTC TCAACCCTAT TGTGAATTTA     360
GAAGAAAACA AGATTTATGG CCTTGTCTCT CACAACCAAG CCATAGGCAT TGCCGTGCTA     420
GAAAAAGGGC GCTTGAACGG GTTTTTGAAC GCCCACAAGC GGTGTGCTTA TAGCGTGATG     480
ATAGGCCAAA ATCAAGTCTT AGGCTTTATA GGGACTAATT TCAAGCAAGA ATTAGTCGTG     540
GATTTCATTG TCCCAAGCGC TGAAATCAAC ATAGGCGATC AAGTGCTAAC GAGCGGGCTA     600
GATGGGATTT TTGGAGCGGG GGTGTTTGTG GGTGAAGTTT CAAGCGTTGA AGATCATTAC     660
ACTTATAAAA GCGCGGTGTT GAAAAACGCT TTTTTAAGCG AAGCCAAACT TTTAAGGCAT     720
GTGTTTTTAA GCGGTGTGAA AAACTAG                                         747
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

```
TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT ATTCTACCTC      60
ATAGGGCGAA AGATTTTAAA AAAGCCTAAA GACGCTCTTT ATGTGGTATT GACTTACGCT     120
TTATTGCCTG GGGTGAATCT CTTTGCGATT TTACTGGCTA AAAGCGTGCT GGTGTTAAGC     180
CTTGGGCTTT TGATTAGCTA TTTGTATATT AAAACCCAAA AAATCCCTTA TTTAACCCTT     240
AGCGCTTGCG CGTTTTTAGA CGGTGCGTTC ATCCCGCTTT TACTAGGGGT TTTTGCCTAC     300
GCTTTAAGGA AAACGGCTAT TTTAAGAGCG CGATCTTTGC TTTGGTGGTT TTAMTTGTGA     360
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

GTGAATTTAA TGGACTATTT TTCTAAAAGT TTGTTTTTAA ATTCATTGAA CACGCAGCGA 60
TTGATCGTCT CCAACAAATT AGCGATTGAC GTGCAATACG GCATGCTCCA AAGTGTCCGC 120
AAAAATTACC CTGATGTGGT GGATGGGGGT GTTAGGGAGG GGCCTTTTTG GGTGTTAGCC 180
GGGGCYTTAA TGCCTTCAAT TTTAATAGAA ATTGGTTATA ATTCCCATGC GATAGAATCT 240
AAACGCATCC AAAGCAAACC GTATCAAAAA ATCTTGGCTA AGGGCATTGC TGATGGCATT 300
GATAGTTTCT TCAGCAAGAA TGATTAG 327

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

TTGGCGTCTC GCTATTCTGT GGCTGTTGGG AATTTATTTT CAGAGCATTT GTATGATTTA 60
AGAAATGAAA CCATGACCAA TCTCATTGGT TTTTTACTGG TGTTGGCGTC CATTTGGGTG 120
TTTTTTTTAG CTCTTGGAGT GTTGCTAGGC AAGATGTTAG TCTTTAGCGG TCTAGGCATT 180
ATAGACAAGG CGTTAGGGTT TATTTTTTCA TGTTTGAAGA CTTTTTTAGT GCTTTCTTTC 240
ATCCTTTATG CGCTCTCTAA AATGGATTTA ATGAAAGACG CTAACGCCTA TTTGCAAGAA 300
AAGAMCRCTA TTTTCCCCAC CATRAAAARC RTCRCTAGTA AGATCATGCG CCTTGATGGC 360
GTCAAACATG TGGAGAAAAA CCTTAAAGAC AACCTTGAAG AAATGAGCGA TGAAGTTAAA 420
AATAAAGGAT CTATTGATAA CGCCAAAGAA TCTTTTAATA AGGGCTACGG ATAA 474

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

```
TTGAGCAAGC AAAGCGCGGA CATTGTGATC ACTAATGACT CCTTAAGCTC TTTAGTCAAA      60
GTTTTAGCGA TCGCTAAAAA AACTAAAAGC ATTACTTGGC AAAATATCTT GTTCGCTTTG     120
GGGATTAAGG CGGTTTTTAT CGTGCTAGGG CTTATGGGGG TAGCGAGCTT GTGGGAAGCG     180
GTCTTTGGCG ATGTGGGGGT TACGCTTTTA GCYTTAGCCA ATTCCATKCG CACGATGAGG     240
GCTTAA                                                                246
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

```
ATGAAAAATT TAAGGCATTT TAGAAAGCTT ATCGCCTTTT TAGGTTTTTC ACCTCTTTTA      60
TTACAAGCGG ATATGACTAC CTTTTTTAAT TCCATTGAAC AACAGCTCAC TAGCCCTACG     120
GCTAAAGGCA TTTTAATGGT TATTTTTTTA GGACTTGCTA TTTTTATATG GAAAAACTTA     180
GATAGATGGA AAGAAATTTT AATGACCGTG CTTGCTTTAA AAGRAGTCCC CATGCAATMW     240
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

```
TTGGCGGGTT TGCYAGTGGG GTGTATRCGG ATGAAACAAA CATTTTGGGR ACTTAGTTGG      60
GGGGAAAAAA GCCAAAAGGT ATGCGTGCAT CGTCCATGGT ATGCTATATG GAGTTGCGAT     120
AAATGGGAGG AAAAAACACA ACAATTTACA GGAAACCAAC TCATCACAAA AACTTGGGCA     180
GGGGGTAATG CGGCTAACTA CTACCACTCT CAAAACAACC AAGACATCAC AGCCAATTTA     240
AAAAATGATA ACGGCACTTA TTTTTTAAGC GGTCTGTATA ACTACACCGG AGGGGAATAT     300
AATGGGGGGA ATTTAGACAT TGAATTAGGC AGTAACGCTA CTTTTAATCT AGGTGCGAGT     360
AGTGGGAATA GCTTCACTTC TTGGTATCCT AATGGGCATA CTGATGTTAC TTTTAGCGCT     420
GGGACTATCA ATGTGAATAA CAGCGTAGAA GTGGGCAATC GTGTGGGATC GGGAGCTGGC     480
ACGCACACCG GCACAGCCAC TTTAAACTTG AACGCTAATA AGGTTACTAT CAATTCCAAT     540
```

```
ATCAGCGCGT ATAAAACTTC GCAAGTGAAT GTAGGCAATG CTAACAGCGT TATTACCATT      600
AATTCGGTTT CTTTAAATGG GGAAACTTGC AGKTCTTTAG CTAGGGTGGG CGTAGGGGCT      660
AATTGCTCCA CTTCTGGGCC TAGCTATTCT TTTAAAGGGA CSACTAACGC TACTAACACS      720
ACTTTTAGCA AWTCAAGCGG SAGTTTCACT TTTGAAGARA ACGCCACTTT TAGCGGGGCG      780
AAATTAAATG GGGGGGCATT CACTTTCAAT AAAAAGTTTA ACGCTACCAA TAATACCGCT      840
TTTAATAGCG GTAGTTTTAC TTTTAAAGGC ACAAGCTCTT TTAATGGTGC GAATTTTAGT      900
AACGCTTCCT ATACTTTTAA TAATCAAGCC ACTTTCCAAA ACAGCTCCTT TAATGGGGGG      960
ACTTTTACTT TTAATTGA                                                    978
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE. DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

```
TTGTTAAGTT TAGTTAAAGG GAAAACCATG CTCCGCTCTC TCTATAGTGC CACTTCAGGG       60
ATGCTCGCCC AACAAACGCA CATTGACACC ACTTCAAACA ACATCGCCAA TGTCAATACC      120
ACCGGGTTTA AAAAATCTCG CGCGGATTTT AACGACTTGT TTTACCAAGC GATGCAATAC      180
GCCGGCACCA ACACAAGCAA CACGACTTTA TCGCCAGATG GCATGGAAGT GGGCCTTGGC      240
GTACGCCCTA GTGCGATTAC CAAAATGTTT TCGCAAGGCA GCCCTAAAGA AACGGAGAAT      300
AATTTAGATA TTGCTATTAC AGGTAAAGGC TTTTTTCAAG TCCAGCTTCC TGATGGCACT      360
ACCGCTTACA CAAGGAGCGG GAATTTCAAG CTAGACGAGC AGGGCAATCT TGTAACAAGC      420
GAGGGCTATC TCCTCATCCC TCAAATCACT TTACCCGAAG ACACCACGCA AGTGAATATC      480
GGTGTGGATG GCACGGTGAG CGTGACTCAA GGCTTGCAAA CGACTTCTAA CGTGATCGGG      540
CAAATCACTT TGGCTAATTT TGTCAATCCG GCGGGGCTTC ATTCTATGGG GGATAATTTG      600
TTTTCCATCA CCAACGCTAG CGGCGATGCG ATTGTGGGCA ACCCGGATTC TCAAGGCTTA      660
GGCAAGTTAA GGCAAGGCTT TTTGGAGCTT AGTAACGTGA GATTGGTAGA AGAAATGACA      720
GATCTAATCA CCGCTCAAAG GGCTTATGAA GCCAATTCTA AAAGCATTCA AACCGCTGAT      780
GCCATGCTCC AAACAGTCAA TTCCCTCAAA CGCTAA                                816
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

```
ATGCAAAATG GGTATTATGC GGCCACAGGG GCAATGGCTA CACAATTTAA CCGCTTGGAT      60
TTAACCTCTA ACAATTTAGC CAACCTAAAC ACCAACGGCT TTAAAAGAGA CGATGCGATT     120
ACAGGCGATT TTTTAAGGCT TTACCAAGAA TACCGAGAGC AACTGCCCTT AGAAGATCAA     180
ACCAAAGCGA GCGCGAAGTA TCTCAACCGC AMCCTCAATC GTGTGCCTAT TCTATCARAA     240
ATCTATACKK ATAGGRAGCT TGGCYGCGTT TGA                                  273
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

```
GTGGGGGCTA TGCCTACTAT CCAAATCCGT GRCTTTGGAG CGGGGGGTTC AGGGCATAGC      60
GATGCGACGC TCATGTTAGT TAATGGTATT CCTGTTTATA TGGCCCCTTA CGCTCACATT     120
GAGCTAGACA TTTTCCCTGT TACCTTTCAA GCCATTGATC GCATTGATGT GATCAAAGGT     180
GGAGGCAGCG TGCAATATGG GCCTAACACT TATGGGGGTA TTGTCAATAT CATCACTAAA     240
CCTATCCCTA ATCAATGGGA AAACCAAGCG GCTGAAAGGA YCACTTATTG GGCTAAGGCT     300
AGAAACGCTG GGTTTGCCGC TCCCCYTGAT AAAACCGGCG ATCCTTCTTT CATCAAGTCT     360
TTAGGCAACA ACCTCCTCTA TAACACTTAT GTGAGGAGCG GAGGGATGAT CAATAAGCAT     420
GTGGGTATCC AGCGCAAGCT AACTGGGTTA GAGGCCAAGG CTTTAGGGAC AATAGCCCCT     480
CTAGTATTTC AAACTATTGG CTGGATGGGG TCTATGACAT CAATGAAAGC AATGGGATTA     540
AAGCCTATTA CCAATACTAC GATTTTGGCT ATCGSCCAAC CGGGA                     585
```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

```
ATGAGAWAGG AGAAAATAAT GACGAATTTT GAAAAGRTTA TCGCGCAAAA CAGGCTCAAA      60
ACGAACGCGG TTTTAACCAC TTACTGCGCG ATTTTTGCTT TTATTGGGTT GTTGGTGGAT     120
GCTATTAGAA TCAACGCTAA TGATTTAGGT ATAGCCCTTT TTAAACTCAT GACTTTTCAA     180
ATTTTTCCTA CGRTTACTAT TGTCATGTTT GTGGTGGCTT TTGTCATTAK KCKKAGTTTG     240
TATCCAAAAT TTTAG                                                      255
```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

```
ATGGRCATGT CTCATATTAT TAAGAGCATT GAAGCTTTAG ATGACTATAC CATTAGATTC      60
ACGCTTAATG GGCCAGAAGC CCCGTTTTTA GCGAATTTGG GCATGGACTT TTTAAGCATT     120
TTGAGTAAGG ATTACGCTGA TTACTTGGCT CAAAATAATA AAAAAGACGA GTTGGCTAAA     180
AAMCCTGTTG GGACAGGGCC TTTCAAATTC TTTTTGTGGA ATAAAAGATG A              231
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

```
TTGATGAGGA AAATTTTTTC TTATATTTCT AAGGTTCTAT TATTTATTGG GGTGGTTTAT      60
GCAGAGCCTG ATTCTAAAGT GGAAGCCTTA GAAGGGAGGA AGCAAGAGTC TTCTTTGGAT     120
AAAAAAATCC GCCAAGAATT GAAGAGTAAG GAATTGAAGA ATAAGGAATT AAAGAACAAG     180
GATTTGAAAA ATAAAGAAGA AAAGAAAGAA ACAAAAGCCA AGAGAAAACC CAGAGCAGAA     240
GTCCATCATG GGGACGCCAA AAATCCCACT CCAAAGATCA CGCCTCCTAA AATCAAAGGG     300
AGTAGTAAGG GCGTTCAAAA TCAAGGCGTT CAAAACAACG CGCCAAAACC TGAAGAAAAA     360
GATACAACCC CTCAAGCTAC TGAAAAAAAT AAGGAAACAA GCCCTAGCTC TCAATTCAAT     420
TCCATTTTTG GTAATCCTAA TAACGCTACC AACAACACCC TTGAAGATAA GGTCGTAGGG     480
GGCATTTCAT TGCTTGTTAA TGGTTCGCCT ATCACGCTGT ATCAAATCCA AGAAGAGCAA     540
GAAAAATCTA AAGTGAGYAA SGCTCRAGCT AGGGATCGTT TGAKTCKCTG A              591
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

```
ATGAAGAGAT CTTCTGTATT TAGTTTCTTG GTAGCTTTTT TATTGGTAGT TGGCTGTAGT      60
CATAAAATGG ATAATAAGAC TGTGGCTGGC GATGTGAGCA CTAAAGCGGT TCAGACTGCG     120
CCTGTTACTA CAGAACCAGC TCCAGAGAAA GAAGAGCCTA AACAAGAGCC AGCTCCAGTG     180
GTTGAAGAAA AGCCGGCTAT TGAAAGCGGG ACTATCATCG CTTCTATTTA TTTTGATTTT     240
GACAAGTATG AGATCAAAGA ATCCGATCAA GAGACTTTAG ATGAGATCGT GCAAAAAGCT     300
AAAGAAAACC ACATGCAAGT GCTTTTGGAA GGCAATACCG ATGAATTTGG CTCTAGCGAA     360
TACAACCAAG CGCTTGGCGT TAAAAGGACT TTGAGCGTGA AAAACGCTTT AGTCATTAAA     420
GGGGTAGAAA AAGATATGAT CAAAACCATC AGTTTTGGCG AAAGCAAACC CAAATGCGTC     480
CAAAAAACTA GAGAATGTTA CAGAGAAAAC AGAAGAGTGG ATGTCAAATT AGTGAAGTAA     540
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

```
ATGGGAACGC TCATTGAAAA ATGGTTTGGC TTCTCTCAAA TCAGAGAAGA ATTAGAAGCT      60
CGCATCAGTG AGTTAGAAGA CGAAAACACC GAATTGTTAA GAGAAAGAGA ATACTTAGCT     120
GCAGAAACTA GCGAGTTAAA AGACGCTAAC GATCAATTAC GGCAAAAAAA CGACAAGTTA     180
TTCATAACAA AAGACAAGCT AACCAAAGAA AACACCGAGT TATTCGCAGA AAACGAAAGC     240
TTATCTGTAA AAATCAGCGG GTTAGAACAC TCTAACGATC AATTATGGCA AAACAATAAC     300
AAGCTCACTA AAGAAAAAGC AGAACTGAAA ACGGAAAAAG ACATTTTAGC TAAAGAAAAC     360
ACACGCTTAT TAGCAGCCAG AGATCGGCTG ACTGAAGAAA AAAGAGAATT GACAACAGAA     420
AAAGAAAGGC TAAAAAGAGA AAACACCGAG CTAACCCATA AAATCACCGA GCTGACTAAA     480
GAAAATAAAG CACTAACCAC CGAAAACGAC AAGCTCAACC ACCAAGTTAC CGCGCTCACT     540
AATGAGCGAG ATAGTCTCGA ACAAGAGCGA GCGCGATTGC AAGATGCGCA TGGGTTTCTA     600
GAAAAACGAT GCACCAATTT AGAGAAAGAA AACCAACGCC TAACTGACAA GCTCAAACAA     660
TTAGAAAGCG CTCAAAAAAG CTTGGAAAAC ACTAACAATC AATTACGGCA AGCTTTAGAA     720
AACTCTAATG TCCAATTAGC ACAAGCTAAA GARARAATWG CCATAGAGRA AAGCGAGCTG     780
GMGCGAAGAA ATCGCACGCT TGAAGAGCTT AGAGGGTATG GAAGCCAAAA GSCGATCTGG     840
ACTTACACAW CAGGCGTTTA G                                               861
```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

GTGTTGCGCA AGCTTTTGGG TAAAAATTGC ATAGAAACGC ATAAGGGGGT GGGCTATCGC 60
TTAACCCACT ATGAAAAAAA ATCCCTCAAA CTCTTTTTAG GGACTTATTT AGGCTCTTCG 120
TTTGTGTTAA TGCTAGTGAT TAGCGTTTTA GCGTTTAACT ATGAAAAAAA CGAAAAAATC 180
AAARTGATAC GCATGGACAT GGACAAAATG GCTTCTAAGA TCGCTAGTGA AATTATCCAA 240
TTGCACATGC AAACGCATGC GGATTATCAC AACGCTTTAA ACGCCCTGAT TTCACGTTAT 300
AAAGACGTTT CCATAGYCCT YTYYGAYACG TAA 333

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

TTGATGACCA AAAGCTTAAA ACTCATTCAA AAAGGGGTTA AAAACCTCTA TGAAACCCTT 60
AAAAATAGGG CTTTAGAGCA TCAAGACACG CTAATGGTGG GCAGAAGCCA TGGGGTGTTT 120
GGCGAACCCA TCACCTTTGG TTTAGTTTTA GCTCTTTTTG CTGATGAAAT CAAACGGCAT 180
TTAAAAGCCC TGGATTTAAC GATGGAATTT ATCRGCGTWG GGGCGATCAG TGGGGCTATG 240
GGGAATTTCG CGCACGCCCC TTTAGAATTA GAAGAATTAG CGTGCGGATT TTTAGGCTTA 300
AAAACCGCTA ATATCAGCAA TCAAGTCATT CAAAGAGACC GCTACGCAGG CTTGCATGCG 360
ATCTGGCTCT TTTAG 375

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

TTGTCAGACG CTTCAAAAAG ATCCCTTAAT CCAACCTTAA TGATGAATAA TAATAATACC 60
CTACCCAAAC CCCTAGAAGA AAGCCTAGAT TTAAAAGAGT TTATCGCTCT TTTTAAAACC 120
TTTTTCGCAA AAGAAAGAGG TTCTATTGCT TTAGAAAACG ATCTCAAACA GGCTTTCACT 180
TATTTAAATG AAGTGGATGC GATCGGTTTG CCTGCCCCCM AAAAGCGTGA AAGAAAGCGA 240
TCTTATTGTT GTCAAACTCA CCAAATTAGG GACGCTCCAT TTAGATGA 288

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

TTGCCTATTA TTTTAYCTGT AATCGTGATG ATGTTTTTTT CCAAAATCGT TGGCGATTTT 60
ATTGAAAAGC ATTATCGCGT CAAAACTTTA GCCTTTGTGT TTTTGCTCGT TGTGGGCGTG 120
TTTTTGTTTT TAGAAGGCTT GCATTTACAC ATCAATAAAA ACTATTTGTA TGCGGGTATT 180
GGTTTTGCCT TGCTCATAGA ATGCTTGRAT ATTTTCATAG AAAAGAAAAT GAAAAAAAGT 240
TAA 243

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

```
ATGATAAAAG CGCGGTTTAA AAAACGCCTT TTAGGATCTA GGGGCGCGTT TGATTTGAAT      60
ATAGACTTAG AAATTAAAGA AGCAGAAGTT GTCGCTTTAT TAGGAGAATC GGGAGCGGGT     120
AAAAGCACGA TCTTACGCAT TTTAGCAGGG CTTGAAGCGG TGAGTAGCGG CTATATTGAA     180
GCCAATCATT CAGTATGGTT AGACACTCAA AAAAAGATTT TTTTAAAACC ACAACAGCGA     240
AAAATCGGCT TTGTGTTTCA AGATTACGCC CTATTCCCTC ATTTAAACGT GTATCAAAAC     300
ATCGCCTTTG CTCACCCTAA AGATAAAAAT AAAATCCACG AAGTGTTACG CTTAATGCGT     360
TTAGAAAACC TAAGCCAGCA AAAAATTCCC AAACTCTCTG GCGGGCAAGC CCAACGAGTC     420
GCTTTAGCAA GAGCTTTAAT CGCAGCCAAA AATCTATTGC TTTTAGATGA GCCTTTAAAC     480
GCCCTAGATA ACGCCTTAAA AAACGAGGTG CAACAAGGTT TGCTTGATTT TATCAAGCGT     540
GAAAATTTAA GCGTGTTATT GGTAAGTCAT GATCCAAACG AAATAACCAA ACTCGCGCGA     600
ACTTTCCTCT TTTTAAACAA TGGCGTTATT GATCCTAATC AAGAAAATCG GCTTTTTTCA     660
AACCGCTTAT TGGTAAAACC TCTCTTTGAA GATGAAAATT ATTGCCATTA TGAGGTCATT     720
CCTCAAACGA TCAGTTTGCC CAAAGATTGT CTGAACCCAA CTTTTAAGCT TGATTTCATT     780
CAAAACAAAA AATTTTAG                                                  798
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

```
GTGAAATTCA GCGTTTTAAC CCTTTTCCCG CAACTCATCT TGCCTTATTT TGAAGATTCT      60
ATTTTAAAAA GAGCGTTAGA AAAAAACCTT TTTGAATTGG AAGTGTTAAA CCTTAGAGAT     120
TTTAGCGCTA ACAAATATCA AAAAGCGGAK TCACACGCTC ATTGGTGGGG GTGCGGGGCA     180
AATTTTAGAC CCTGA                                                     195
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

```
TTGTGGCGCA CACCGAAGAC RCCCTTAGTC ATTAAACCCT ATTTGAAAAG CATGAGCGAT      60
TCAGAGATYT TTGCGGYCAY GTGCGTGGGY ATGGCYAGCG TTRCGGGGCC TGTGTTAGCC     120
```

```
GGGTATGCGA GCATGGGCAT TCCTTTACCT TATTTAATCG CCGCATCGTT TATGTCCGCT     180
CCTGGGGGGT TGCTGTTCGC TAAAACCATT TACCCGCAAA ACGAAACCAT TTCTAGCCAT     240
GCAGATGTTT CTGCAGAAGA GCATGTCAAT ATTATAGAAG CTAYCGCWMA TGGGGCAAGC     300
ACAGGGGYTC ATTTAGCCTT GCATGTGGGG GCGATGCTTT TAGCCTTTGT GGGGATGGTC     360
GCGCTCGTTA ACGGGCTTTT AGGGGTTGTA GGGGGATTTT TAGGCATGGA GCAT           414
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

```
GTGATGAACT TTTTTGTGGG CGGACTTTCC ATTGTTTGTA ATGTGGTGGT CATCACTTAC      60
TCCGCGCTCC ACCCTACAGC CCCTGTAGAA GGTGCAGAAG ATATTGTTCA AGTATCGCAC     120
CATTTGACCA GTTTCTATGG GCCAGCGACT GGGTTATTGT TTGGKTTTAC CTACTTGTAT     180
GCCGCTATCA ACCACACTTT TGGTTTGGAT TGGAGACCCT ATTCTTGGTA TAGCTTATTC     240
GTAGCGATCA ACACTGTTCC TGCTGCGATT TTATCCCACT ATAGCGATAT GCTTGATGAC     300
CACAAAGTGT TAGGCATCAC TGAAGGCGAT TGGTGGGCAA TCATATKG                  348
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

```
GTGCTTTTGG GCAAGCATAG TGGGGCGGGG TTGTTGAGCG CTTTAWGCGC GTTAAGTTTT      60
GGATCTGGGG TGGTGAGTAT CCAAGCGTTA GAGTGCGAGA TAACTTCTAA TAACAAGCCT     120
TTAGAATTGG TTTTTTGTGA AAATTTCCCT AAAAAGCTCA GCGCGTTCGC TCTTGGCATG     180
GGGTTAGAAA ATATTCCAAA GGATTTTAAG AAGTGGCTTG AATTAGCCCC ATGCGTTTTA     240
GATGCGGGCG TTTTTTATCA TAAAGAAGTG TTACAAGCCT TAGAAAAAGA AGTGATCTTA     300
ACCCCTCACC CTAAAGAGTT TTTATCGTTA TTGAAATCAG TGGGGATCAA TATAAGCATG     360
CTAGAATTAC TAGACAATAA ACTAGAAATC GCAAGGGATT TTTCTCAAAA ATACCCCAAG     420
GTGGTTTTGC TTTTAAAGGG GGCTAATACC CTAATCGCTC ATCAAGGGCG GGTTTTTATC     480
AACAATTTAG GGAGCGTGGC TTTRGCCAAA GCAGGCAGTG GCGATGTGTT AGCGGGGCTG     540
ATTGTAAGCC TACTTTCTCA AAACTACACG CCTTTAGRCG CCGCSATTAA CGCAAGTTTG     600
```

GCGCACGCCC TAGCGGGTTT ARAATTTAAG AATMATTAMG CTTTAACGCC CSTAGATTTG 660
ATAGAAAAGR TCAAACGACT ATAA 684

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

GTGCYTTTAT ACCTAGCACT AACCTTGAGT TTAGGCATTG CTATGCTTTT AGTGGAAATG 60
CTGATTGGAA ATTTGGGTAA AAAAGACGTT GTTTCCAATT ATCAAATCTT AGATCCTAAA 120
AGGAAAAAAT ATTACCCTTT CACTTCTTTT TTTATTTTAG GCGGCCCTCT CATTCTATCT 180
TTTTTATGCGG TGGTGTTAGG CTGGGTGCTT TACTATCTTT TTGTAGTAAC TTTTGATTTG 240
CCTAAAGATT TAGMGCAGGC TAAAATGCAR TTCMGMATGC TTCAAAATGG CAGTTTGATC 300
TGGCCTGTTA TTGACTTTAG CGCATGCT 328

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

TTGACAACAA AAGCGTGTTG GTTGCTTCGG GTTTGTTGTT ATAGAAGTCT AAATATTACA 60
ATCAAGGATA GAACGATGAA AACCAATGGT CATTTTAAGG ATTTTGCATG GAAAAAATGC 120
TTTTTTAGGCG CGAGCGTGGT GGCTTTATTA GTGGGGTGTA GCCCGCATAT TATTGAAACC 180
AATGAAGTTG CTTTGAAATT GAATTACCAT CCAGCTAGCG AGAAAGTTCA AGCGTTAGAT 240
GAAAAGATTT TACTTTTAAG GCCAGCTTTC CAATACAGCG AKAATATTTG CTAA 294

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

```
TTGAGTGAGT GGCAAACATT TTGTTTAAAA GATTTAGGGA AAATAGTCGG CGGCGCTACC      60
CCACCTACCA ATAACCCCAA AAATTATGGC AATAAAATTG CTTGGATTAC CCCTAAAGAT     120
TTATCCACTT TACAAGGGCG CTACATTAAA AAAGGCAGCC GCAGCATTTC ACGATTAGGG     180
TTTAAATCAT GCTCTTGTGT GTTGCTCCCA AAGCATGCCA TTTTATTTTC TTCAAGAGCT     240
CCCATAGGTT ATGTGGCAAT TGCTGAAAAA AGGCTATGCA CCAATCAAGG TTTTAAAAGT     300
ATTATCCCTA ACAAAAAAAT TTATTTTGAA TTTTTATATT ACTTATTAAA ATACTATAAG     360
GATAACATTT CCAACATAGG GGGCGGAACT ACTTTTAAAG AAGTTTCAGG GGCTACTTTA     420
GGKTCTATTC CAAGTTAA                                                  438
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

```
ATGGAATTTA TGAAAAAGTT TGTAGCTTTA GGGCTTCTAT CCGCGGTTTT AAGCTCTTCG      60
TTGTTAGCCG AAGGTGATGG TGTTTATATA GGGACTAATT ATCAGCTTGG ACAAGCCCGT     120
TTGAATAGCA ATATTTATAA TACAGGGGAT TGCACAGGGA GTGTTGTAGG TTGCCCCCCA     180
GGTCTTACCG CTAATAAGCA TAATCCAGGA GGCACCAATA TCAATTGGCA CTCCAAATAC     240
GCTAATGGGG CTTTGAATGG TTTTGGGTTG AATGTGGGTT ATAAGAAATT CTTCCAATTC     300
AAGTCGCTAG ATATGACAAG CAAGTGGTTT GGTTTTAGAG TGTATGGGCT TTTTGATTAC     360
GGGCATGCCG ATTTAGGTAA ACAAGTTTAT GCACCTAATA AAATCCAGTT GGATATGGTC     420
TCTTGGGGTG TGGGGAGCGA TTTGTTAGCT GATATTATTG ATAAAGACAA CGCTTCTTTT     480
GGTATTTTTG GTGGGGTCGC TATCGGCGGT AACACTTGGA AAAGCTCTGC AGCAAACTAT     540
TGGAAAGAGC AAATCATTGA AGCCAAAGGT CCTGATGTTT GTACCCCTAC TTATTGTAAC     600
CCTAATGCCC CTTATAGCAC CAACACTTCA ACCGTCGCTT TTCAAGTGTG GTTGAATTTT     660
GGGGTGAGAG CCAATATCTA CAAGCATAAT GGCGTGGAAT TTGGCGTGAG AGTGCCGCTA     720
CTCATCAATA AATTTTTGAG CGCGGGTCCT AACGCTACTA ACCTTTATTA CCATTTGAAA     780
CGGGATTATT CGCTTTATTT GGGGTATAAC TACACTTTTT AA                        822
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

```
TTGGTCCAAA TCGTAGTCGT GTTTTATGGT TTGCCCCCCC TTGGGGTCTA TATGGATCCA      60
ATCCCGGCAG GCATTATTGC GTTTTCTTTT AATGTGGGGG CATACGCTTC AGAGACTTTG     120
AGGGCGAGCT TTCTTTCTGT CCCTAAAGAT CAATGGGATT CAAGCTTGAG TTTGGGCTTG     180
AATTACTTGC AAACCTTTTG GCATGTCATC TTTTTTCAAG CGCTCAAAGT CGCCACGCCA     240
AGCCTAAGTA ACACTTTCAT CAGCCTTTTT AAAGAAACTT CTTTAGCGTC TGTGGTCACT     300
ATCGCAGAGG KTTTTAGAAT CGCACAGCAA AAAGYGAACG TCAGCTATGA CTTTYYGCCT     360
ATTTATTTGG AAGKCGCTTT GATTTACTGG CTTTTTTGCT TGGTTTTAGA AGTGATTCAA     420
AAGCGCGTGG AAAAAATCTT AAATTAA                                         447
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

```
GTGGTGGCTG ATGAAGTTAG GAATTTAGCT GGGCGCACTC AAAAGTCTTT AGCCGAAATC      60
AATTCCACTA TCATGGTGAT TGTCCAAGAA ATCAATGATG TGAGTTCGCA AATGAATCTC     120
AATTCGCAAA AAATGGAGCG CTTGAGCGAT ATGAGTAAAA GCGTGCAAGA AACTTACGAA     180
AAAATGAGTT CTAATTTAAG CTCAGTCGTT TTAGACAGCA ATCAAAGCAT GGACGATTAC     240
GCTAAATCCG GACACCAAAT TGAAGCTATG GTAAGCGATT TTGCAGAAGT GGAAAAAGTG     300
GCTTCTAAGA CTTTGGCTGA TTCTTCAGAT ATTTTAAACA TCGCTACGCA TGTGAGTGGA     360
ACGACCATGA ATTTAKACAA ACAAGTGAAT TTGTTTAAAA CTTAA                     405
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

```
ATGAATTACG ATAACTATTG GGATGAGGAC AAACCAGAAC TCAATATCAC GCCTTTAGTG      60
GATGTGATGC TTGTTTTATT GGCTATTCTT ATGGTAACGA CGCCCACTCT CACCTATAAA     120
GAAGAGATTG CCTTGCCTTC TGGTTCAAAA ACTGCTAGAG CCACTCAAGA TAAAGTGATA     180
GAGATACGCA TGGATAAAGA CGCAAAAATC TATATAGATA GTCAAACCTA TGAATACAMC     240
TCTTTCCCGG ACACTTTCAA TTTGCTTTCT AAAAAATACG ATAAAGATAC TAGGGTGAGT     300
ATCCGTGCGG ACAAGCGATT GACCTATGAC AAAGTGATTT ATTTGTTAAA AACGATTAAA     360
GAAGCGGGGT TTTTGAAAGT TTCTTTAATC ACAAGTCCTT AA                        402
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

```
ATGCCACCCA CACSCCCCCA AGCGAGTATT TTAAGGCTAA CCCTAAAAAA CCCTTTGMGC      60
MTGCTATCTC GTTATTCGCT CTGTCTGTTG AAAAAAACGC GCTTGCAAAC AACATCAAAC     120
AGCGCACCAA AAGCATGCTT GATTGCGGGC TTATTGAAGA AATCAAAGCC CTTTATATTA     180
AATACCCTAA AGATTCGCAG CCTTTTAAAG CCATAG                               216
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

```
ATGCCTGTTA TAAGAGTTTT AGTAATGCTT GCAACAATGA TGATGAAATT AGTAAAAACG      60
GCAAAAGAAA AGAAAGTTTT TAAGAATGTG GGAATATCTA TAATGGGGAT TGCTTTTTGG     120
GAAGCGATAA AAGACTCGAT AAAAAAACAA ATTAAAAAAA GCGATTGGAT ATGCGGGAAT     180
GTTAAGACTG CGGATGATTA TTTAAAAACG CATCCTAACT CATGGTTTAA TTCAGCAATA     240
GGTGTAACAG CGATAACAGC CATGCTTATG AATGTGTGTT TTGCTGATGA CCAATCCAAA     300
AAAGAAGTGG CTCAAGCTCA AAAGGAAGCT GAAAACGCTA GGGATAGAGC GAACAAGAGT     360
GGGATAGAAC TGGAACAAGA AGAGCAAAAG ACAGAACAAG AAAAACAAAA GACAGAACAA     420
GAAAAACAAA AGACAGAACA AGAAAAACAA AAGACAGAAC AAGAAAAACA AAAGACAGAA     480
CAAGAAAAAC AAAAGACAAG CAATATAGAG ACTAACAATC AAATAAAAGT AGAACAAGAA     540
CAACAAAAGA CAGAACAGGA AAAACAAAAG ACAAACAATA CGCAAAAAGA TTTGGTTAAC     600
AAAGCAGAAC AAAATTGCCA AGAAAATCAT AATCAATTCT TTATTAAAAA TTAA           654
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

```
ATGGTTATTT CTGGGCATTT CACCACTTAT AGCTATATTG AGCCTTTTAT CATTCAAATC      60
AGCCAATTTT CTCCTGACAT TACAACGCTA ATGTTGTTTG TGTTTGGGTT AGCAGGCGTG     120
GTGGGGAGTT TTTTGTTCGG CCGTTTGTAT GCGAAAAATT CAAGAAAATT TATCGCTTTT     180
GCAATGGTTT TAGTCATTTG CCCGCAACCT CTTGCTTTTT GTGTTTAA                  228
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

```
ATGAAATCTA CAAGAATTGG TTCTAAAATT GTCATGATGG TGTGTGCGGT TGTTATTGTC      60
ATTAGCGCTG TTATGGGCGT TATTATCAGC TACAAGGTTG AAAGCGTGTT GCAAAGCCAA     120
GCCACAGAAT TGCTGCAAAA AAAAGCTCAG TTAGTCAGTT TTAAAATTCA AGGCATTATG     180
AAGCGCATTT TTATGGGCGC TAACACCCTT GAAAGGTTTT TAAGCGATGA AAATGGCGCT     240
ATTAATGACA CCCTAAAAAG ACGCATGCTC TCTGAGTTTT TGTTAGCAAA CCCTCATGTG     300
```

```
TTATTGGTTA GCGCGATTTA TACGAATAAT AATGAACGAA TGATCACTGC AATGAACATG     360
GATTCAAAAA TCGCCTACCC TAATACCGCA CTCAATGAAA ACATGACCMA CCCAATCCAT     420
TCGCTCAAAA GTATAACCCG TTCARATCCC TATTATAAAG AGGTTAATGM CRATAAAATC     480
TATRRCATRR ACATTACCCT CCCCCTAATR RRCAARAATY AAAATRTTAT ARRCRCWCTW     540
AATTTCKTTT TAAACATTGA CWGCTTTTTA TACTGM                               576
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

```
ATGGCATACA AATATGATAG AGACTTGGAA TTTTTAAAGC AACTGGAATC TAGTGATTTA      60
TTGGATTTGT TCGAGGTGCT TGTTTTTGGT AAAGACGGCG AAAAAAGACA CAATGAAAAA     120
CTCACAAGCT CCATAGAATA CAAAAGGCAT GGCGATGATT ACGCTAAATA CGCAGAAAGA     180
ATCGCTGAAG AGTTGCAATA CTATGGGAGC AATAGTTTTG CGAGTTTCAT TAAAGGTGAA     240
GGAGTCTTAT ACAAAGAGAT TTTATGCGAT GTGTGCGATA AATTAAAGGT CAATTACAAC     300
AAGAAAACTG AAACGACTTT AATTGAACAA AACATGCTTT CTAAAATCTT AGAAAGAAGC     360
CTAGAAGAAA TGGATGATGA AGAAGTGAAA GAAATGTGCG ATGAATTGTC CATAAAAAAC     420
ACGGACAATT TGAACAGACA AGCCTTAAGC GCGGCGACTT TAACGCTGTT TAAAATGGGA     480
GGCTTTAAAT CTTATCAATT AGCTGTCATT GTTGCGAATG CGGTTGCAAA AACCATTCTA     540
GGGCGTGGTT TATCGCTTGC GGGCAATCAA GTGCTTACAA GAACTCTGAG CTTTTTAACA     600
GGCCCTGTTG GCTGGATCAT TACAGGCGTA TGGACAGCGA TTGATATTGC AGGGCCGGCT     660
TATAGGGTAA CCATACCGGC ATGCATTGTG GTCGCCACTT TACGCCTAAA AACGCAACAA     720
GCCAATGAAG ATAAGAAGTC GTTGCAAATA GAATCCGTTT AA                        762
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

```
TTGTTGCTTT TTATCGTTGT GATCACCTCT TTGGTTAAAA ACACGATCCC AAATATTTGG      60
CTCACTAAAA TCCTTTATAT GGCTATCTTG CTTTGCGCGA TCGCTCATTC TGTGGGGCYA     120
ATCTTGCGYT GGTATGTGAG TGGGCATTCG CCTTGGAGTA ACGCTTATGA GTCCATGTTC     180
```

```
TATATCGCAT GGGCTTCTGT TATCGCAGGG TTTGTTTTAC GAMCTAAACT CGCGCTATCG     240
GCTTCTAGCT TTTTGGCCGG TATCGCGCTC TTTGTGGCTC ATTTAGGCTT TATGGACCCT     300
CAAATTGGCC CTTTAGTGCC GGTGTTAAAA TCCTATTGGC TCAATATCCA TGTCTCTGTC     360
ATCACCGCTA GTTATGGCTT TTTGGGCTTG TGTTTTGTGC TAGGGATTTT AAGTTTGGTT     420
TTGTTTATTT TGCGCAAACA AGGGCGTTTC AATTTAGACA AAACCATTCT TTCCATTAGC     480
GCTATCAATG AAATGAGCAT GATTTTAGGC CTGTTCATGC TCACAGCCGG GAATTTCTTA     540
GGTGGGGTGT GGGCGAATGA ATCTTGGGGG CGCTATTGGG GGTGGGACCC TAAAGAAACT     600
TGGGCGTTGA TTTCTATTTG CGTCTATGCC TTGATCTTGC ATTTGCGTTT TTTAGGCTCT     660
CAAAATTGGC CCTTTATTTT AGCGAGCAGC AGCGTGCTAG GGTTTTATTC GGTTTTAATG     720
ACTTTATTTT GGCGTGAATT ACTACCTTTC TGGCTTGCAC AGCTATGCCG CAGGKSATCS     780
TTTGCCGATC CCTACTTTTT TATACTTTTT GGTAGCGATA CCTTTCGCTC TCGTATCTTG     840
GCGTATTTCA AACGTCATTT GAGTTTGCCT AAATTGGTTT AA                        882
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```
GTGGAAATGA TCCACACGCA AGATTACATT AAAATGGAAG AAGCCGCCAC TGAGGCGATT      60
AAGCGTAAGG AATCTTCCAT TTACTTGGGC ATGGATATTT TAAAAAATGG GGCTGACGCT     120
TTGATTTCAG CGGGGCATAG CGGGGCGACT ATGGGTTTAG CGACCTTGCG TTTAGGGCGT     180
ATCAAGGGGG TTGAAAGGCC TGCTATTTGC ACTTTAATGC CTAGCGTTGG CAAACGCCCT     240
AGCGTGCTAT TAGACGCAGG AGCGAACACG GATTGCAAGC CTGAATATTT GATTGATTTT     300
GCTCTCATGG GGTATGAATA CGCTAAAAGC GTGTTGCATT ATGACAGCCC TAAAGTGGGT     360
CTTTTGAGTA ATGGTGAAGA AGATATTAAG GGGGGAATAC GCTCGTTAAA GAAACGCATA     420
AAATGTTGA                                                             429
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

```
ATGCTAGAAA TCAAGAATTT AAACTGCGTT TTAAACTCTC ATTTTTCGCT CCAAAACATC      60
```

```
AATATTTCTT TAAGTTATAG TGAAAGGGTG GCGATCGTGG GCGAAAGCGG GAGCGGGAAA      120
AGCTCTATCG CTAATCTCGT CATGCGATTA AACCCTAGAT TCAAGTCCCA TAATGGCGAA      180
ATCCTGTTTG AAACAACCAA TCTTTTAAAG GAAAGCGAAG CGTTYMTGCA GCATTTAAGG      240
GGGAATATTA TCGCTTACAT CGCCCAAGAC CCCCTATCCA GCCTCAACCC CTTGCATAAA      300
ATCGGCAAGC AAATGAGTGA AGCCTATTTT TTACACCATA AAAACGCTTC TCAAGTGTCT      360
CTTAATGAAC AAGTTTTAAA CGTTATGAAA CAAGTTCAAT TGGATGAAAA TTTTTGGAAT      420
GTTTCTCTTA TGT                                                         433
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

```
ATGAACTACA AAGTTGCATC TGCTAGAAAT ATCGCAACGC TTCTTTTCTT ATTCTTTTCT       60
CAAAGTGAAG CTTTTGATTT GGGTAAAATC GCTAAAATCA AAGCGGGTGC TGAAAGTTTC      120
TCTAAAGTCG GTTTCAATAA CAAACCTATC AACAMTAATA AAGGGATTTA CCCTACCGAA      180
ACCTTTATGA CGATTAATGG CTTACATGCA GGTGGATTTT ACGGAGCTCT TGCCCAAAAG      240
CGCTACGGCT AA                                                          252
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

```
ATGGACGCTT TAGAAATCAC CCAAAAACTC ATCAGTTACC CTACCATTAC GCCCAAAGAA       60
TGCGGTATTT TTGAATACAT TAAATCGCTT TTTCCTGCTT TTAAAACCCT AGAATGTGAA      120
AAAAATGGCG TGAAAAACCT TTTTTTATAC CGCATTTTTA ACCCCCTCAA AAAGCATGCA      180
GAAAAAGAAC ATGCAAAAGA AAAGCATGTR AAAGAAAATG TTAWGCCCTT GCATTTTTGC      240
TTKGCAGGGC ATATTGRTGT CGTGCCTCCT GGGRRCAWTK GGCRRRSKGA TTCCTTTWWA      300
YCCATCATTA AAGAGGGGTT TTTATACGGT CGTGGGGCGC AAGACATGAA GGGGGGCGTT      360
GGGSSGTTTT TKAGGTGCRR GTTWAAATTT TAA                                   393
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1023 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

```
ATGATTTTAA GCATTGAAAG TTCTTGCGAT GACAGCTCTT TAGCCCTTAC AAGAATAGAG      60
GACGCCAAGC TCATCGCTCA TTTTAAAATC TCTCAAGAAA AGCACCACAG CTCTTATGGG     120
GGCGTTGTGC CTGAGATTGC ATCGCGCCTG CATGCTGAGA ATTTGCCGCT TTTATTAGAA     180
CGCGTTAAAA TAAGCTTGAA TAAGGATTTT TCCAAAATTA AAGCCATCGC TATCACTAAT     240
CAGCCAGGTT TGAGCGTTAC TTTAATAGAG GGTTTGATGA TGGCAAAAGC CTTGAGCTTG     300
TCTTTGAATT TACCCTTGAT TTTGGAAGAT CATTTGAGAG GGCATGTGTA TTCGCTCTTT     360
ATCAATGAAA AACAAACCCG CATGCCTTTA AGCGTGCTGC TAGTCTCTGG GGGGCATTCT     420
TTAATTTTAG AGGCTAGAGA TTATGAAGAC ATTAAAATCG TTGCCACGAG TTTAGACGAT     480
AGCTTTGGGG AGAGTTTTGA TAAGGTTTCA AAAATGCTTG ATTTAGGCTA TCCAGGAGGC     540
CCCATAGTGG AAAAATTAGC CCTTGATTAT GCACACCCAA ACGAGCCTTT AATGTTCCCT     600
ATCCCTTTAA AAAACAGCCC GAATTTGGCT TTTAGTTTTT CAGGTTTAAA AAATGCGGTG     660
CGTTTGGAGG TTGAAAAAAA CGCCCATAAT TTGAACGATG AGGTAAAACA AAAGATTGGC     720
TATCATTTTC AAAGCGCGGC TATCGAGCAT TTAATCCAGC AGACTAAACG CTATTTTAAA     780
ATCAAACGCC CTAAAATTTT TGGCATTGTG GGGGGAGCGA GCCAAAATCT AGCCTTAAGA     840
AAGGCGTTTG AGGATTTGTG TGCTGAGTTT GATTGCGAGC TTGTTTTAGC CCCTTTAGAA     900
TTTTGCAGCG ACAATGCCGC CATGATAGGG CGATCAAGCC TAGAAGCTTA TCAAAAAAAG     960
CGCTTTATCC CTTTAGAAAA AGCCGATATT TCGCCAAGAA CGCTGTTAAA AAATTTTGAG    1020
TGA                                                                  1023
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

```
ATGTTATCTT CTAATGATTT GTTTATGGTC GTTTTAGGGG CGATTTTATT GGTGTTGGTG      60
TGCTTGGTGG GGTATTTGTA TCTTAAAGAA AAAGAGTTTT ACCATAAAAT GAGGCGTTTA     120
GAAAAAACTT TAGATGAATC CTATCAAGAA AATTATCTCT ATTCTAAGCG TTTGAGAGAA     180
TTAGAGGGGC GTTTGGAAGG CCTTTCTTTA GAAAAAAGCG CTAAAGAGGA CAGCTCATTA     240
AAAACGACTC TTTCGCACCT TTATAACCAG TTGCAAGAAA TCCAAAAATC CATGGATAAA     300
```

```
GAGCGCGATT ACTTAGAAGA AAAAATCATT MYTTRGAAAA CAAWTTTWAA GACATGGGGC      360
ATTATGCCGC TAGCGATGAA GTCAACGGAA AAACAGGTTT TGAAAATGTA TCAAGAAGGC      420
TATAGCGTGG ATTCTATTTC TAAAGAATTT AAAGTGAGTA AGGGCGAGGT GGAATTTATA      480
TTGAACATGG CAGGGTTAAA ATGGTAG                                          507
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

```
TTGGATCCCT TTAGCCATAA GGAGAATTTT TTAGCCGTTG AAACCTTTAA AATGCTAGGC       60
AAAACAGAAA GTAAAGACAA TCTTAATTGG ATGATCGCTT TGATCATTGA AAAAGACAAG      120
GTCTATGAGC AAGTGGGATC GGTGCGTTTT GTGGTGGTTG TAGCGAGTGC TATCATGGTG      180
TTAGCCTTAA TCATAGCGAT CACTCTTTTA ATGCGAGCGA TCGTGAGCAA TCGTTTGGAA      240
GTCGTTTCTA GCACCTTGTC TCATTTCTTT AAATTATTGA ACAATCAAKC CCATTCTAGC      300
RACAYTAAAT TGGTTRAAGC GCGATCTAAT GACGAATTAG GGCGCAYGCA AACASCTGAT      360
YAATAA                                                                 366
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```
ATGGAATTTT ATCAAGTCTA TGACCCATTA GGCCATATTT GGCTGAGCGC TTTAGTCGCA       60
CTTTCGCCTA TTGCGCTCTT TTTTATCTCT CTTATTGTCT TTAAACTTAA AGGGTATAGC      120
GCTGGGTTTT TAAGCTTAGC GCTTTCAATC CTTATTGCGT TATTTGTGTA TAAAATGCCT      180
GTTCAAATGG TGAGCGCGAG TTTTTTCTAT GGCTTTCTTT ATGGCTTGTG GCCGATCGCA      240
TGGATTGTGA TCGCTGCGAT TTTTCTTTAC AACCTTTCAG TGAAGTCCGG GTATTTTGAG      300
ATTTTAAAAG AAAGCATTTT AAGCTTGACG CCGGATCATC GCATTTTAGT GATTTTGATC      360
GGGTTTTGTT TTGGCTCGTT TTTAGMMGGC GCGRTTGGTT TTGGAGGCCC GGTAGCRATC      420
ACAGCGGCGA TTTTAGTGGC CTTGGGCTAA                                        450
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

```
ATGAAAAGAA TTTTAGTTTC TTTGGCTGTT TTGAGTCATA GCGCGCATGC TGTCAAAACT      60
CATAATTTGG AAAGGGTGGA AGCTTCAGGG GTGGCTAACG ATAAAGAAGC GCCTTTAAGC     120
TGGAGGAGCA AGGAAGTTAG AAATTATATG GGTTCTCGCA CGGTGATTTC TAACAAGCAA     180
CTCACTAAAA GCGCCAATCA AAGCATTGAA GAAGCTTTGC AAAATGTGCC AGGCGTGCAT     240
ATTAGAAACT CTACCGGTAT TGGAGCTGTG CCTAGCATTT CCATTAGGGG GTTTGGTGCT     300
GGAGGCCCAG GGCATTCTAA TACGGGAATG ATTCTAGTCA ATGGGATTCC TATTTATGTC     360
GCGCCCTATG TTGAAATTGG CACGGTTATT TTTCCTGTAA CCTTTCAGTC TGTGGATAGA     420
ATCAGCGTAA CTAAGGGTGG GGAGAGCGTG CGTTATGGCC CTAACGCTTT TGGCGGTGTG     480
ATCAACATCA TCACCAAAGG CATTCCTACC AATTGGGAAA GTCAGGTGAG CGAGAGGACC     540
ACTTTTTGGG GCAAGTCTGA AAACGGGGGC TTTTTCAATC AAAATTCTAA AAACATTGAT     600
AAAAGCTTAG TTAATAACAT GCTTTTTAAC ACCTATTTAA GAACGGGGGG TATGATGAAT     660
AAGCATTTTG GAATCCAAGC TCAAGTCAAT TGGCTCAAAG GGCAAGGGTT TAGATACAAC     720
AGCCCTACGG ATATTCAAAA TTACATGTTA GATTCATTGT ATCAAATCAA TGATAGCAAT     780
AAAATCACCG CTTTTTTTCA ATATTATAGT TATTTCTTGA CAGACCCTGG ATCTTTAGGC     840
ATAGCCGCTT ACAATCAAAA TCGTTTTCAA AACAACCGCC CCAATAACGA TAAAAGCGGG     900
AGAGCGAAGC GATGGGGAGC TGTGTATCAA AACTTTTTTG GGGACACGGA TAGGGTAGGG     960
GGGGGATTTC ACTTTTAG                                                  978
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

```
TTGCGTTCAA TTTCAAGGAT AAAGATGCTT TCAGTGTATG AAAAAGGGAA TGCCCTAGAC      60
AAAAGGGTGC TTGAAGAATG GCTTTTAAGC GAAGACATTT TAATGGAAAA CGCCGCTATG     120
GCTTTAGAAA GGGCGGTTTT ACAAAACGCT TCTTTGGGCG CTAAGGTCAT TATTCTTTGT     180
GGGAGTGGGG ATAATGGAGG TGATGGCTAT ACTCTAGCCA GGCGTTTAGT GGGGCGTTTT     240
AAAACGCTGG TCTTTGAAAT GAAATTAGCA AAAAGCCCCA TGTGCCAATT GCAAAAAGAA     300
AGGGCTAAAA AAGTAGGGGT AGTCATCAAA GCATGGGAAG AAAAGAATGA AGATTTAGAA     360
```

```
TGCGATGTGT TAGTAGATTG CGTGGTAGGG AGCGCTTTTA AGGGCGGATT AGAGCCGTTT     420
TTAGATTTTG AAAGCCTTTC TCAAAAAGCA CGCTTTAAAA TCGCTTGCGA CATTCCTAGC     480
GGGATAGATT CTAAAGGCAG GGTGGATAAG AGGGCGTTTA ARGSCGGATA CCGACTATCA     540
GCATGGGCGC TATTCAAGTC ATGCTTACTA AGCRATAARR CTAAARACTA TATARRRRAA     600
TTGAAARTRR RRCATTTARR RGTTTTTAAT CAAATTTATG AGATCCCAAC ARACACTTTT     660
TTACTMGAAA AAARCGATTT GAARCTGCCC TTAAGGGATA GAAAGAAACG CTCACAAAGG     720
CGATTACGGG CATGCGCATG TGCTTTTGGG CAAGCATAG                            759
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

```
ATGGCATTAG ACAAAAGGAT TTGGATGCAY TTTGATCTTT TGCCTTTTGT GTTTATCATC      60
CCCTTGTTGG TGGTTTCTTT TTTGTTGATT TTTGAGAGTA GTGCGGTTTT GAGCTTGAAG     120
CAAGGGGTTT ATTATGCCAT AGGGTTTCTT CTCTTTTGGG TAGTGTTTTT TATCCCTTTC     180
AGGAAACTCG ATCGGTGGCT CTTTGCGCTT TATTGGGCGT GCGTTATTTT ATTAGCGTTA     240
GTGGATTTTA TGGGATCGAG CAAGCTTGGA GCGCAGCGAT GGCTAGTCAT TCCTTTCACT     300
TCTATCACCT TACAGCCTAG CGAGCCTGTG AAAAATCGCY ATTCYTTTAT TGTTGGCGCA     360
TTTGAKYAAA ATYAACCCGA CCYCCTTTTA AGGGCTATGA TTGGGGCATG TTTTTAA       417
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

```
GTGTTAATGG CGTTGARCGA TAAACGCTAC GGCTTAGAAG CAGGGATCAA GTATTTCACC      60
ATGGGGGCGA TGGCGAGCGC GTTTTTTGCT ATGGGCGCGA TGGCTTTTTA CCTGCTTACA     120
GGGAGCTTGA ATCTTGAAGT CATTACCCTA TACTTACACA CTGAGGGCAT CACAAACCCC     180
ATGCTCTTTG CGATGGGCAC TATTTTTTTG ATTGGAGCGA TTGGCTTTAA GGTTTCTTTA     240
GTGCCTTTCC ATACCTGGAT GCCTGATGTG TATGAGGGYA ATAACCCAGT CTTTGCGAGC     300
TATATTTCCA TTGTGCCTAA AATCGCTGGC TTTGTGGTAG CGACTCGCCT TTTTGGGGCG     360
TTTATAGACA CTCATACCGC TTGGGTAGAA GACATTTTTT ATGTTTTGAT CCTTATGACT     420
```

```
ATCACCATCC CTAATTTCAT TGCTTTATGG CAAGAAGATG TCAAAAGGAT GCTCGCTTAT      480
AGTTCTATTT CGCATTCTGG GTTCGCTTTA GCGTGCGTGT TTATCCACAC TGAAGATAGC      540
CAACAAGCGA TGTTTGTTTA TTGGTTCATG TTTGCCTTCA CTTACATTGG GGCTTTTGGC      600
CTTTTATGGC TCTTAAAAAG CCGGGAAAAA ACATGGGATG AACGCTACGA TCACCCCTAT      660
TCTAAATTCA ACGGCCTTAT CAAAACCCAC CCCTTAGTGG CGATCTTGGG CGCTATTTTT      720
GTTTTTGGGC TTGCAGGGAT CCCGCCTTTT AGCGTGTTTT GGGGGAAATT TTTAGCCGTT      780
GAAAGCGCGT TAGAGAGCAA TCACATTCTT TTAGCGGTGG TGATGTTAGT TAATAGCGCG      840
GTGGCTGCGT TTTATTATTT CCGTTGGCTC GTGGCGATGT TTTTCAATAA GCCCTTACAA      900
ACCCAAAGCT ACGCCAAAAC GATATTTACA CCCAAAACGC CACCATGCCC ATTTATGCGG      960
TCATTATTGC CATGGCGTTA G                                                981
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

```
ATGATAAACT CAAAGAAAAG CTTGAAAAAG GGCTTAAGGG GCTTTTTTAA AATTTTAAAG       60
GACAGAAATG GCGCACATTT TAGTTGCGGA GCGACTTCAG GGTTTGGGCT AGAAATCGCT      120
AAGGCGTTTT TACAAAAAAA CCATGTGGTT TTTGGCACAG GGAGGCGGCA AGAGAATTTA      180
CAAAAATTGC AGCTCGCTTA CCCTAAGCGT TTCATTCCCC TGTGTTTTGA TCTTCAAAAC      240
AAGCCTGAAA CTAAGCGAGC GATAGAAACT ATTTTTTCCA TGACGGATCG CATTGACGCT      300
TTAATCAATA ACGCCGGCTT AGCGCTAGGC TTGAACAAGG CTTATGAATG CGAGTTAGAC      360
GACTGGGAAG TCATGATAGA CACGAATATC AAGGGGTTGT TGCATCTCAC CCGCTTGATC      420
TTGCCCTCTA TGATAGAGCA TGACCAAGGG ACTATCATCA ATCTTGGTTC TATCGCTGGC      480
ACTTACGCCT ATCCTGGAGG GAAKGTCTAT GGAGCGAGCA AGGCGTTKGT GAAACAAYYY      540
TCTYYAAATT TGCGAGCGGA CGTGGCTGGC ACTAACACTA GAGGGAGAAG GTGGAACCCG      600
GGGTGTGTGG CGAAACCGAA AGTCAGCAGG GTGCGGGGTA AAGGCGATAA ACCAAAGCCC      660
AAATCCGGCT ATGAAAAACA CCCCTTACCC CAAACCACAA GACAAGGGCT AACATCGGGC      720
TAG                                                                    723
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

GTGAGCGGGG TGGTGTTAAG CAAATTTGAT AGCGATTCTA AAGGGGGTAT CGCCTTAGGC 60
ATCACTTATC AATTGGGCTT ACCCTTGCGT TTTATTGGGA GTGGGGAAAA AATCCCTGAT 120
TTAGACGTGT TTATGCCTGA AAGGATTGTG GGGCGTTTGA TGGGGGCTGG AGATATTATC 180
TCGCTCGCTG AAAAAACCGC CAGCGTTTTA AACCCTAATG AAGCCAAAGA TTTAAGCAAA 240
AAGCTCAAAA AAGGGCAATT CACTTTCAAC GATTTTTTAA ACCAAATTGA AAAAGTGAAA 300
AAATTAGGCT CTATGAGTTC TCTRATCTCT ATGATTCCAG GTTTAGGGAA TATGGCAAGC 360
GCGCTAAAAG ACACGGATTT AGAAAGTTCT TTAGAAGTGA AAAAAATCAA GGCCATGGTT 420
AATTCCATGA CGAAAAAAGA GCGAGAAAAC CCCGAGATTT TAAACGGCAG CCGAAGAAAA 480
AGGATCGCTT TAGGGARCGG CTTAGAAGYG YCTGAAATCA ATCGCATCAT CAAACGCTTT 540
GATCAGGCGA GCAAAATGGC GAAACGACTC ACGAATAAAA AGGGTATTAG CGATYTGATG 600
AATCTAWCGA KCTAG 615

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

GTGGAAAAAG CCCATCCGGA TGTGTTTAAC CTCTTGTTAC AGGTTTTAGA TGAGGGGCAT 60
TTAACCGATA GTAAGGGCGT GAGGGTGGAT TTCAAAAACA CGATTTTGAT TTTAACCAGC 120
AATGTGGCTA GCGGCGCGCT TTTAGAAGAG GATTTGAGTG AAGCCGATAA ACAAAAAGCG 180
ATCAAAGAGA GCCTGAGACA ATTCTTCAAG CCGGAATTTT TAAACCGCTT AGATGAAATC 240
ATCTCCTTTA ACGCCCTAGA TAGTCATGCT ATCATCTAA 279

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

TTGGTGTTTT TAGACAGGCG TTTGATTGTG ATGGTTACGG ACTCTAAAGG GAGTCGTTAT 60
ATTAATGTGC ATATCTTATT CCGCCAAATC AGTTTGTATG CGCTGTTGAG CGTTGTGGGA 120
TCTTTATTGT TTTTAGGCGT TTCATTACTG GTTTTAAATA AAGAAATTAA AAACATTGAA 180

AAACAGCATG CTTTAMTCAC TAAGGAATTT GAGAAAAAAA GAGAGACGAA TGAAMAGCTT 240
TCTTYG 246

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

TTGAGTTTGA TGASTGTGTT AAATGCCAAA GAATGCGTTY CGCCCATAAC AAGAAGCGTT 60
AAGTATCATC AGCAAAGTGC SGAGATCAGA GCCTTGCAAT TACAAAGTTA CAAAATGGCG 120
AAAATGGCGC TAGACAATAA CCTTAAGCTC GTTAAAGACA AAAAGCCAGC CGTCATCTTG 180
GATTTAGATG AAACCGTTTT GAACACTTTT GATTATGCGG GCTATTTAGT CAAAAACTGC 240
ATTAAATACA CCCCAGAAAC TTGGGATAAA TTTGAAAAAG AAGGCTCTCT TACGCTCATT 300
CCTGGAGCGC TAGACTTTTT AGAATACGCT AATTCTAAGG GCGTTAAGAT TTTTTACATT 360
TCTAACCGCA CCCAAAAAAA TAAGGCATTC ACTTTAAAAA CGCTCAAAAG CTTTAAGCTC 420
CCCCAAGTGA GTGAAGAATC CGTTTTGTTA AAGGAAAAAG GCAAGCCTAA AGCCGTTAGG 480
CGGGAGTTAG TCGCTAAGGA TTATGCGATT GTTTTACAAG TGGGCGACAC TTTGCATGAT 540
TTTGACGCCA TTTTTGCTAA AGACGCTAAA AACAGCCAAG AACAACAAGC CAAAGTCTTG 600
CAAAACGCTC AAAAATTCGG CACAGAATGG ATCATTTTAC CCAACTCTCT TTATGGCACA 660
TGGGAAGATG GGCCTATAAA AGCATGGCAA AATAAAAAAT AA 702

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

ATGTTGGCGG CTGGTTTGAC TTTGCCTGAA TTTGGGTGTT ATTTAAGCCA TTATCTTTTA 60
TGGAAAGAAT GCGTCAAATT AGATCAACCG GTCGTTATTT TAGAAGATGA TGTAACGCTA 120
GARTCTCATT TCATGCAAGC CTTAGAAGAT TGTTTGAAAA GCCCTTTTGA TTTTGTGAGA 180
CTCTATGGGT GTTATTGGTA TTACCAACGA GACAAAATTC CATGTTTTGC CCAAAGAATT 240
TGTATTTCCT CCCTTTGA 258

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

```
TTGATCGCTT TGAGAGTAAC GGCTTGGAAR GTGGYGGCCA TGAAACGCTT GCATTTGAGC      60
GTGAAAGACG CTGAAAACTT TGATGCGATC CTCAGAGAGA GACCCTTTTT TAAAGATTTG     120
ATAGAGTTTA TGGTGAGTGG TCCGGTGGTG GTTATGGTTT TAGAAGGCAA AGATGCGGTG     180
GCTAAAAACA GAGAGCTTAT GGGAGCGACT GATCCCAAAC TCGCCCAAAA AGGTACTATC     240
AGAGCGGATT TTGCTGAGAG CATTGACGCT AATGCGGTGC ATGGGAGCGA TAGCTTGGAA     300
AACGCGCACA ATGAAATCGC TTTCTTTTTT GCCGCTAGAG AGTTTTAA                  348
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

```
TTGATGTGGC TCAAAACGCT TACACTTCAA ACGCTCAATA CCGACAAAGC CTTGCAAGAA      60
TTTTCTAAAA CGATGGAGGC GTTTAAAACC AAACTCATCC AATCCGCTAA CGATGTGCAT     120
TCAGAGACTT CTCGCGCCGC TATCGCTAAC GATTTAGAAC GCTTAAAAGA GCATATGATA     180
AATGTCGCTA ATACCTCCAT AGGGGGGGAA TTTTTATTTG GAGGCAGTAA GGTGGATAGA     240
CCCCCCATTG ATAGTAATGG GAAATACCAT GGCAATGGCG AAGATTTAAA CGCGCTTATT     300
AGCTCTGATA ACCTTGTGCC TTATAATATC AGCGGGCAAG ATTTGTTTTT AGGCACCGAT     360
AAAGACAAAC ACAAACTCAT TACCACCAAC ATTAAATTAC TCAATCAAAA CAAGCTCCAM     420
CCTGATGTGA TGGACGCTTT AGAGCATTCT TCATTGCCTG AAGAAGTTTT CATTAAACCC     480
AGCGATACCT TGCGAGAACT CATCGGCGAT AACGATAAAA ACCCCACCAA TGACCCTAAA     540
GAGTTTTTTT ATTTGCAAGG CATTAGGCCT GATGGCTCTA GTTTTAAAGA AAAATTCGCG     600
TTGGATAAAG CCTATCAAAA CCAAGAAAGC GCGACTAAAG TGAGCGATTT GTTGGATAAA     660
ATCGGGCATG CTTACGGGAA CACTTCGCAA AATAAAGTCG TGGATGTGAG TTTGAACAAT     720
TGGGGGCAAA TTGAGATTAA AAACCTAACC CCCGGCAGTG AAAATTTGGA TTTTCATTTG     780
ATTTCTAGCG ATGGGGATTT TGACGATTTA GACGCCTTGC GTTCGAGCGG TAAAAGGGTT     840
ACTGAATATG TCAAAAGCGC GTTTGTAACG GATAGGAGTT TGAGCCAAGT TAAAGCGGTG     900
CCTAACATGT ATAACCCTAA AGTGCTTGAA ATCCCTAGCG TGTTTGTGAC TAAAGACAAT     960
GTTTTAGCTA ACAAAAACAC CAAGTTGAGC GAGATTTTTG GMGATAAGGT GGAAACTTTA    1020
```

```
AAAATCAACG CCAGCCGTTT GGGCGATGAA AGCGCTATTA AAATCCCAAA CCTCCCTATT    1080
AATTTGGATA TTCCCATTCT TTTAGATGTG AAAAACTCTA CGATTAAAGA TTTGAAAGAC    1140
GCGATTAAAG AACGCTTCAA TAATGAAGGT GGATGTGGAA ATTGA                    1185
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

```
TTGAAGGCAT TAAACGACTG CATGGTATTT TTTCATAAGA AAATTATTTT AAATTTTATC      60
TATTCTTTAA TGGTTGCTTT TTTATTCCAT TTATCCTATG GGGTTCTTTT AAAAGCCGAT     120
GGAATGGCTA AAAAGCAAAC TCTTTTAGTG GGTGAAAGGC TTGTGTGGGA TAAGCTCACG     180
CTGTTAGGGT TTTTAGAAAA AAACCATATC CCCCAAAAAC TCTACTACAA TTTGAGCTCT     240
CAAGATAAAG AATTGAGTGC TGAAATCCAA AGCAATGTTA CCTACTACMA CTTTAAGAGA     300
TGCAAATAA                                                            309
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

```
ATGAAATTTT TTCTTTTAAA GAAATTCAGC RAATTTTTAA ACACTCAAAC GCATTTTAAC      60
CTCAAACGCT TGAACGCGTC TAGTTTTTTA TTAGAGACTT TTTCTAAAGA AAAACACGCC     120
TTTGTTGTGG ATTTGAGCGC GCCTTATATT GGTTTGTCCA AAAAACCCCC AGAGAGCGTT     180
TTAAAAAACA CTTTAGCGTT AGATTTTTGT TTGAATAAAT TCACCAAAAA CGCCAAAATT     240
TTACAAGCAA ACGTCATTGA TAACGATCGG ATTTTAGAAA TCAAGGGCGC TAAAGATTTA     300
GCTTATAAGA GTGAAACTTT TATTTTGCGT TTAGAAATGA TCCCTAAAAA AGCCAATCTC     360
ATGATTTTAG ATCAAGAAAA ATGCGTGATA GAGGCTTTTC GTTTTAATGA CAGGGTGGCT     420
AAAAACGATA TTTTAGGGGC ATTGCCTCCT AATATTTACG AGCATCAAGA AGAGGATTTG     480
GATTTTAAGG GATTGTTGGA CATTTTAGAA AAAGATTTTT TATCCTATCA GCACAAAGAA     540
TTGGAACACA AAAAAAATCA AATCATCAAG CGATTAAACG CCCAAAAAGA ACGCTTGAAA     600
GAAAAATTAG AAAAACTAGA AGATCCTAAA ACTTTACAGC TGGAAGCGAA AGAATTGCAA     660
ACTCAAGCCT CATTGTTGCT CACTTACCAG CATTTAATCA ACAGGCGTGA AAATCGCGTG     720
```

```
ATTTTAAAGG ATTTTGAAGA TAAAGAATGC ATGATTGAAA TTGATAAGAG CATGCCCTTA     780
AACGCTTTTA TCAATAAAAA ATTCACTCTC AGCAAGAAAA AGAAACAAAA ATCGCAATTC     840
TTGTATTTAG AAGAAGAGAA TCTGAAAGAA AAAATCGCTT TTAAGGAAAA TCAAATCAAC     900
TATGTTAGAG ACGCTGCAGA AGAAAGCGTT TTAGAAATGT TTATGCCGGT AAAAAACTCT     960
AAAATCAAAC GCCCGATGAA CGGGTATGAA GTGCTGTATT ATAAGGATTT WAAAWCGGGT    1020
TTRGGAAAAA CCAAAAAGAG AATATCAAGC TTTTACAAGA CGCAARARCG AATGATTTKT    1080
GGATGCAYKT GA                                                        1092
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

```
Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
1               5                  10                  15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
            20                  25                  30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
        35                  40                  45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
    50                  55                  60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
65                  70                  75                  80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
                85                  90                  95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
            100                 105                 110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
        115                 120                 125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
    130                 135                 140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
145                 150                 155                 160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

```
Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1               5                  10                  15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Xaa
            20                  25                  30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
        35                  40                  45
Tyr Gln Asp Glu Ile Ala Lys Xaa Gln Arg Gln Lys Ser
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

```
Leu Xaa Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1               5                  10                  15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
            20                  25                  30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
        35                  40                  45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
    50                  55                  60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65                  70                  75                  80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
                85                  90                  95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
            100                 105                 110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
        115                 120                 125
Ile Arg Asn Asn Xaa Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
    130                 135                 140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
145                 150                 155                 160
Pro Thr Glu Ile Gly Xaa Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
                165                 170                 175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
            180                 185                 190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
        195                 200                 205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
    210                 215                 220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225                 230                 235                 240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
                245                 250                 255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
            260                 265                 270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

```
Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
1               5                  10                  15
Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Xaa Ala Val Ser Leu
            20                  25                  30
Xaa Val Leu Ala Leu Val Met Gly Ser Ser Xaa Gly Leu Glu Glu Phe
        35                  40                  45
Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

```
Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1               5                  10                  15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
            20                  25                  30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
        35                  40                  45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
    50                  55                  60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65                  70                  75                  80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
                85                  90                  95
Ile Leu Leu Pro Xaa Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
            100                 105                 110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

```
Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1               5                  10                  15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
            20                  25                  30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His
        35                  40                  45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Xaa Gly Xaa Asp Met Val
    50                  55                  60
Xaa Xaa Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Xaa Trp
65                  70                  75                  80
Cys Xaa Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
                85                  90                  95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
            100                 105                 110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
        115                 120                 125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
    130                 135                 140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
145                 150                 155                 160
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
                165                 170                 175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

```
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1               5                  10                  15
Leu Ala Lys Glu Leu Ala Leu Asn Leu Xaa Leu His Phe Glu Arg Phe
            20                  25                  30
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
        35                  40                  45
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
    50                  55                  60
```

```
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
65                  70                  75                  80
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Xaa Asn
                85                  90                  95
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
            100                 105                 110
Ile Leu Ile Met Thr Xaa Xaa Val Gly Ser Lys Asp Lys Asp Thr Leu
        115                 120                 125
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
    130                 135                 140
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
145                 150                 155                 160
Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
                165                 170                 175
Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
            180                 185                 190
Pro
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

```
Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1               5                   10                  15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
            20                  25                  30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
        35                  40                  45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
    50                  55                  60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65                  70                  75                  80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
                85                  90                  95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
            100                 105                 110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
        115                 120                 125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
    130                 135                 140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145                 150                 155                 160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
                165                 170                 175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
            180                 185                 190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
        195                 200                 205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
    210                 215                 220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225                 230                 235                 240
```

```
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
                245                 250                 255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Xaa Asn Asp Ser Asp Gly
            260                 265                 270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Xaa
        275                 280                 285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

```
Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1               5                  10                  15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val
            20                  25                  30
Glu Met Ile Xaa Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
        35                  40                  45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
    50                  55                  60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65                  70                  75                  80
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
                85                  90                  95
Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
            100                 105                 110
Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Xaa Thr Leu
        115                 120                 125
Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
    130                 135                 140
Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
145                 150                 155                 160
Lys
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

```
Val Cys Leu Gly Leu Ala Asp Val Met Val Val Leu Ser Leu His Leu
1               5                  10                  15
Asn Leu Asn Pro Thr Asn Pro Lys Trp Leu Asn Arg Asp Arg Leu Val
            20                  25                  30
Phe Ser Gly Gly His Ala Ser Ala Leu Val Tyr Ser Leu Leu His Leu
        35                  40                  45
Trp Gly Phe Asp Leu Ser Leu Asp Asp Leu Lys Arg Phe Arg Gln Leu
    50                  55                  60
His Ser Lys Thr Pro Gly His Pro Glu Leu His His Thr Glu Gly Ile
65                  70                  75                  80
Glu Ile Thr Thr Xaa Phe Arg Ala Arg Phe Cys
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

```
Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1               5                  10                  15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
            20                  25                  30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
        35                  40                  45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
    50                  55                  60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
65                  70                  75                  80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
                85                  90                  95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
            100                 105                 110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Xaa Ser Thr Glu Leu
        115                 120                 125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
    130                 135                 140
Asp Phe Gly Phe Leu Thr Phe Xaa Thr Pro Thr Arg Gly Ser Phe Phe
145                 150                 155                 160
Tyr Asn Ala Xaa Thr Thr Thr Ala Asn Phe Lys Asp Tyr Xaa Val Val
                165                 170                 175
Gly Xaa Xaa Phe Glu Xaa Ala Thr Trp Arg Ala
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

```
Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1               5                  10                  15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
            20                  25                  30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
        35                  40                  45
Phe Val Xaa Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
    50                  55                  60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65                  70                  75                  80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Xaa Trp His Lys
                85                  90                  95
Glu Asn Arg Thr Ser Phe Ser Gly
            100
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

```
Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1               5                  10                  15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn
            20                  25                  30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
        35                  40                  45
Asp Phe Val Ile Cys Leu Leu Leu Leu Xaa Gly Ile Leu Met Gly Val
    50                  55                  60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
65                  70                  75                  80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
                85                  90                  95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
            100                 105                 110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
        115                 120                 125
Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
    130                 135                 140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
145                 150                 155                 160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
                165                 170                 175
```

Ile Leu Thr Pro Pro Leu
180

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1 5 10 15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
20 25 30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
35 40 45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
50 55 60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
65 70 75 80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
85 90 95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Xaa Glu Gln
100 105 110
Phe Xaa Ala Gln
115

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1 5 10 15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
20 25 30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
35 40 45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
50 55 60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Xaa Xaa Xaa Asp Gly Gly

65 70 75 80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
85 90 95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
100 105 110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
115 120 125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
130 135 140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg
145 150 155 160
Leu Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu
165 170 175
Leu Thr Gln Xaa Gln Phe Cys Val Ile Pro Thr Tyr Gln Leu Leu Gln
180 185 190
Glu Lys Gly Pro Asp His His Lys Glu Phe Glu Met Ala Leu Tyr Ile
195 200 205
Gln Asp Lys Met Tyr Ala Thr Ala Lys Gly Lys Ser Lys Lys Glu Ala
210 215 220
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

Leu Leu Val Leu Leu Asn Leu Lys Xaa Thr Pro Asn Leu Met Trp Pro
1 5 10 15
Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly Val Asn Met
20 25 30
Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
35 40 45
Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
50 55 60
Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
65 70 75 80
Trp His Xaa Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
85 90 95
Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
100 105 110
Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
115 120 125
Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
130 135 140
Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Xaa Asp
145 150 155 160
Xaa Val Gln Thr Leu Ser Ser Xaa Phe Ser Val Val Leu Ile Leu Pro
165 170 175
Ser Xaa Gly Thr Ala Ile Asn Met Leu Leu Xaa Met Arg Gly Gln Trp
180 185 190
His Gln Xaa Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
195 200 205
Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys

210 215 220
Ser Val Asn Ala
225

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

Met Lys Ala Pro Ser Gln Xaa Asp Leu Lys Lys Ile Leu Gly Ile Glu
1 5 10 15
Glu Val Ile Xaa Xaa Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
20 25 30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
35 40 45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
50 55 60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
65 70 75 80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
85 90 95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
100 105 110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
115 120 125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
130 135 140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145 150 155 160
Met Ser

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1 5 10 15

Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
20 25 30
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
35 40 45
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
1 5 10 15
Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
20 25 30
Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
35 40 45
Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
50 55 60
Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
65 70 75 80
Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
85 90 95
Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
100 105 110
Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
115 120 125
Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
130 135 140
Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
145 150 155 160
Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
165 170 175
Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
180 185 190
Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
195 200 205
Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
210 215 220
Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
225 230 235 240
Leu Val Ala Ser Phe Lys Met Val
245

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

```
Leu Leu Val Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu
1               5                  10                  15
Arg Lys Ala Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr
            20                  25                  30
Thr Asn Thr Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu
        35                  40                  45
Lys Arg Glu Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe
    50                  55                  60
Phe Ser Arg Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe
65                  70                  75                  80
Ser Gly Ser Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val
                85                  90                  95
Lys Lys Glu Lys Arg Lys Glu Val Arg Ile Glu Lys Lys Glu Glu Arg
            100                 105                 110
Ile Asp Ala Arg Glu Asn Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys
        115                 120                 125
Glu Pro Lys Lys Ala Asn Gln Gly Thr Glu Asn Ala Pro Thr Leu Glu
    130                 135                 140
Glu Lys Xaa Tyr Gln Lys Ala Glu Arg Lys Phe Asp Ala Lys Xaa Xaa
145                 150                 155                 160
Arg Arg Ser Phe Lys Xaa
                165
```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

```
Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
1               5                  10                  15
Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
            20                  25                  30
Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
        35                  40                  45
Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
    50                  55                  60
Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
65                  70                  75                  80
Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
                85                  90                  95
Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
            100                 105                 110
Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
```

115 120 125

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Xaa Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

Met Ala Leu Arg Val Leu Leu Phe Phe Cys Phe Leu Phe Leu Gln Ala
1 5 10 15
Glu Asp Lys Ser Gln Glu Leu Ser Ser Ile Gln Lys Gln Met Ala Leu
20 25 30
Val Asp Lys Lys Leu Ala Lys Asp Asp Asn Val Trp Leu Lys Lys Phe
35 40 45
Glu Asn Tyr Lys Ile Tyr Asn Gln Ile Tyr Thr Glu Lys Glu Ser Val
50 55 60
Arg Gln Glu Leu Arg Arg Leu Lys Asn Lys Lys Ser Lys Asp Leu Leu
65 70 75 80
Lys Ile Ser Thr Leu Glu His Thr Leu Lys Ala Leu Glu Ser Gln Gln
85 90 95
Lys Met Phe Glu Ser Tyr Gly Val Asn Pro Phe Lys Asp Leu Ile Glu
100 105 110
Arg Pro Asn Ile Pro Asn Ile Pro Asn Ile Ala Asn Pro Ile Ala Ile
115 120 125
Ile Asp Gly Ile Ser Phe Ile Lys Ser Met Arg Leu Lys His Glu Asn
130 135 140
Leu Lys Asn Asn Gln Thr Ser Leu Gly Glu Val Leu Lys Leu Leu Asp
145 150 155 160
Gln Lys His Gln Leu Leu Asn Gln Trp His Ala Leu Asp Lys Ser Ala
165 170 175
Lys Leu Ser Asp Glu Ile Tyr Gln Thr Gln Ala Lys Arg Leu Glu Leu
180 185 190

```
Gln Gly Ala Gln Asn Ile Leu Lys Thr Thr Ile Gly Ile Phe Gln Lys
        195                 200                 205
Asp Ser Asp Glu Ala Ile Ser Ile Val Lys Ser Gln Val Lys Asn Gln
    210                 215                 220
Leu Phe Lys Leu Val Tyr Val Phe Leu Ala Ala Leu Leu Ser Val Val
225                 230                 235                 240
Phe Ala Trp Ile Leu Lys Ile Ile Ser Ser Lys Tyr Ile Glu Asn Asn
                245                 250                 255
Glu Arg Val Tyr Thr Val Asn Lys Ala Ile Asn Phe Val Asn Val Ser
            260                 265                 270
Val Ile Xaa Xaa Ile Xaa Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr
        275                 280                 285
Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Xaa Met
    290                 295                 300
Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly
305                 310                 315                 320
Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp
                325                 330                 335
Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His
            340                 345                 350
```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

```
Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
1               5                  10                  15
Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
            20                  25                  30
Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
        35                  40                  45
Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
    50                  55                  60
Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
65                  70                  75                  80
Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
                85                  90                  95
Phe Ile Leu
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

```
Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1               5                  10                  15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
            20                  25                  30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
        35                  40                  45
Glu Lys Asp Met Glu Tyr Phe His Xaa Ser His Xaa Trp Ile Thr Xaa
    50                  55                  60
Tyr Leu Xaa Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

```
Leu Gly Leu Val Xaa Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
1               5                  10                  15
Lys Ile Ser Val Phe Leu Gly Xaa Asn Leu Met Leu Tyr Pro Val Xaa
            20                  25                  30
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala
        35                  40                  45
Thr His Ala Gly
    50
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

```
Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1               5                  10                  15
```

```
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
                20                  25                  30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
            35                  40                  45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu
        50                  55                  60
Gly Thr Asp Thr Gly Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln
65                  70                  75                  80
Lys Thr Asn Ala Thr Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val
                85                  90                  95
Lys Glu Leu Val Lys Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu
            100                 105                 110
Asn Gly Asn Ser Ile Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala
        115                 120                 125
Ala Ala Val Thr Asn Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro
    130                 135                 140
Ile Thr Gln Leu Ile Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn
145                 150                 155                 160
Gly Leu Val Ala Arg Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu
                165                 170                 175
Phe Gln Trp Leu Phe Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser
            180                 185                 190
Lys Thr Ile Ile Gly Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp
        195                 200                 205
Val Ser Pro Phe Ile Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala
    210                 215                 220
Met Asp Gly Arg Arg Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr
225                 230                 235                 240
Leu Gly Asp Pro Lys Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr
                245                 250                 255
Ala Arg Lys Arg Asn Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr
            260                 265                 270
Asp Leu Leu Ala Cys Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro
        275                 280                 285
Thr Lys Ile Phe Leu Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln
    290                 295                 300
Arg Leu Ala Asn Val Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly
305                 310                 315                 320
Leu Asp Arg Lys Ile Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile
                325                 330                 335
Ala Ser Phe Asn Leu Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu
            340                 345                 350
Ser Thr Asp Thr Val Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn
        355                 360                 365
His Ser Ile Ile Asp Lys Tyr Gln Pro
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

```
Met Lys Leu Val Ser Leu Ile Val Ala Leu Val Phe Cys Cys Phe Leu
1               5                   10                  15
```

```
Gly Ala Val Glu Leu Pro Gly Val Tyr Gln Thr Gln Glu Phe Leu Tyr
            20                  25                  30
Met Lys Ser Ser Phe Val Glu Phe Phe Glu His Asn Gly Lys Phe Tyr
        35                  40                  45
Ala Tyr Gly Ile Ser Asp Val Xaa Xaa Ser Lys Ala Lys Lys Asp Lys
    50                  55                  60
Leu Asn Pro Asn Pro Lys Leu Arg Asn Arg Ser Asp Lys Gly Val Val
65                  70                  75                  80
Phe Leu Ser Asp Leu Ile Lys Val Gly Glu Gln Ser Tyr Lys Gly Gly
                85                  90                  95
Lys Ala Xaa Asn Phe Xaa Asp Gly Lys Thr Xaa His Val Arg Val Thr
            100                 105                 110
Gln Xaa Ser Asn Gly Asp Leu Xaa Phe Thr Ser Ser Tyr Xaa Lys Trp
        115                 120                 125
Gly Tyr Val Gly Lys Thr Phe Thr Trp Lys Arg Leu Ser Asp Glu Glu
    130                 135                 140
Ile Lys Asn Leu Lys Leu Lys Arg Phe Asn
145                 150
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

```
Leu Glu Thr Leu Phe Leu Val
1               5
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

```
Met Xaa Thr His Asp Arg Arg Lys Leu Arg Ile Xaa Leu Thr Gln Thr
1               5                   10                  15
Thr Thr Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu
            20                  25                  30
Leu Gly Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser
        35                  40                  45
Ala Ser Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala
```

```
    50                  55                  60
Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
65                  70                  75                  80
Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
                85                  90                  95
Asp Ile Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
            100                 105                 110
Lys Ala
```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

```
Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1               5                  10                  15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
            20                  25                  30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
        35                  40                  45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
    50                  55                  60
Lys Gln Gln
65
```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

```
Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Xaa Val
1               5                  10                  15
Leu Ala Met Val Xaa Met Leu Ile Xaa Ser Leu Ala Asn Ile Phe Phe
            20                  25                  30
Asn Tyr Leu Phe Ile Phe Xaa Leu Glu Val Gly Val Gln Gly Xaa Ala
        35                  40                  45
Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
    50                  55                  60
```

```
His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
65                  70                  75                  80
Phe Ile Phe Ser His Phe Phe Ser
                85
```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

```
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1               5                  10                  15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
            20                  25                  30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
        35                  40                  45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
    50                  55                  60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65                  70                  75                  80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
                85                  90                  95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
            100                 105                 110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
        115                 120                 125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
    130                 135                 140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145                 150                 155                 160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
                165                 170                 175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
            180                 185                 190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
        195                 200                 205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
    210                 215                 220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225                 230                 235                 240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
                245                 250                 255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Xaa Ala
            260                 265                 270
Lys Lys Ser Pro
        275
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

```
Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
1               5                  10                  15
Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
            20                  25                  30
Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
        35                  40                  45
His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
    50                  55                  60
Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Xaa Leu Ser Lys
65                  70                  75                  80
Xaa Phe Lys Xaa Ser Gly Leu Trp Gly Lys Asn Gly Arg
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

```
Met Ala His His Xaa Glu Gln His Gly Gly His His His His His His
1               5                  10                  15
His Thr His His His His Tyr His Gly Gly Glu His His His His His
            20                  25                  30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
        35                  40                  45
His Gln Glu Glu Gly Cys Cys His Gly Xaa His Glu
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

```
Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1               5                  10                  15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
            20                  25                  30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
        35                  40                  45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
    50                  55                  60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65                  70                  75                  80
Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
                85                  90                  95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
            100                 105                 110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
        115                 120                 125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
    130                 135                 140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145                 150                 155                 160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
                165                 170                 175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
            180                 185                 190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
        195                 200                 205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
    210                 215                 220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225                 230                 235                 240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
                245                 250                 255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
            260                 265                 270
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
        275                 280                 285
Asp Xaa Xaa Gly Glu Ile Thr Gly Phe
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

```
Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1               5                  10                  15
Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
            20                  25                  30
```

```
Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
        35                  40                  45
Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
    50                  55                  60
Ile Thr Phe Phe Ala Ala Xaa Arg Leu Gly Xaa Ser Arg Leu Ser Tyr
65                  70                  75                  80
Asp His Glu Leu Leu Val Phe Phe Leu Xaa
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

```
Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1               5                  10                  15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
            20                  25                  30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
        35                  40                  45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
    50                  55                  60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65                  70                  75                  80
Pro Met Lys Ile Gln Lys
                85
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

```
Val Tyr Ser Arg Phe Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala
1               5                  10                  15
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Thr
            20                  25                  30
Leu Leu Gln Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala
        35                  40                  45
Thr Ala Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala
```

```
    50                  55                  60
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser
65                  70                  75                  80
Thr Asn Phe Lys Ser Asn Ser Gln Ser Gln Val Ala Leu Lys Asn Gly
                85                  90                  95
Ala Ser Ser Gln His Leu Phe Asn Ala Asn Ala Thr Trp Lys Arg Val
            100                 105                 110
Ile Ile Met Gly Thr Leu His Thr Phe Ile Cys Met Trp Glu Phe Tyr
        115                 120                 125
Lys Ser Ser Leu Thr Leu Asp Arg Met Met Trp Arg Leu
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

```
Met Xaa Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1                   5                   10                  15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
            20                  25                  30
Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
        35                  40                  45
Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
    50                  55                  60
Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
65                  70                  75                  80
Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
                85                  90                  95
Lys Gly Asn Val Xaa Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
            100                 105                 110
Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
        115                 120                 125
Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Xaa Gly Leu
    130                 135                 140
Ser Glu Ser Tyr Xaa Tyr Gly Leu Gly Val Glu Lys Xaa Xaa Lys Lys
145                 150                 155                 160
Ala Glu Glu Tyr Met Gln Lys Ala Cys Asp Phe Asp Ile Asp Lys Asn
                165                 170                 175
Cys Lys Lys Lys Asn Thr Ser Ser Arg
            180                 185
```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

```
Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
1               5                  10                  15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
            20                  25                  30
Ala Arg Xaa Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
        35                  40                  45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
    50                  55                  60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65                  70                  75                  80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
                85                  90                  95
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
            100                 105                 110
Trp Asp Phe His Phe Phe Xaa Val Tyr Val Tyr His Leu Phe Phe Glu
        115                 120                 125
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

```
Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1               5                  10                  15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
            20                  25                  30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
        35                  40                  45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
    50                  55                  60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65                  70                  75                  80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
                85                  90                  95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
            100                 105                 110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
        115                 120                 125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
    130                 135                 140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
145                 150                 155                 160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
                165                 170                 175
```

```
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
            180                 185                 190
Phe
```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

```
Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile
1               5                  10                  15
Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp
            20                  25                  30
Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
        35                  40                  45
Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
    50                  55                  60
Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65                  70                  75                  80
Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
                85                  90                  95
Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
            100                 105                 110
Ser Phe Xaa Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
        115                 120                 125
Pro
```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

```
Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val
1               5                  10                  15
Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys
            20                  25                  30
Glu Pro Leu Tyr Leu Val His Ser Glu Leu Leu Glu Arg Ala Asn Gln
```

```
        35                  40                  45
Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile
    50                  55                  60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser
65                  70                  75                  80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu
                85                  90                  95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn
            100                 105                 110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp
        115                 120                 125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly
    130                 135                 140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser
145                 150                 155                 160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu
                165                 170                 175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe
            180                 185                 190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys
        195                 200                 205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys
    210                 215                 220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg
225                 230                 235                 240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
                245                 250                 255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
            260                 265                 270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
        275                 280                 285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
    290                 295                 300
Tyr Leu Ala
305
```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

```
Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Xaa Cys
1               5                   10                  15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
            20                  25                  30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu
        35                  40                  45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
    50                  55                  60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu
65                  70                  75                  80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
                85                  90                  95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
```

```
            100                 105                 110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Xaa Glu
        115                 120                 125
Arg Glu Asn Phe Xaa Xaa Gln Arg Ala Phe Val Xaa Xaa Xaa Xaa Ala
    130                 135                 140
Lys Ala
145
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

```
Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1               5                  10                  15
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
            20                  25                  30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
        35                  40                  45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
    50                  55                  60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65                  70                  75                  80
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
                85                  90                  95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
            100                 105                 110
Gln Asn Tyr Gln Glu Ala Xaa Asp Ala Tyr Ala Arg His Ala Phe
        115                 120                 125
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

```
Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1               5                  10                  15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
            20                  25                  30
```

```
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
        35                  40                  45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
    50                  55                  60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65                  70                  75                  80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Xaa Asp Leu
                85                  90                  95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Xaa Xaa
            100                 105                 110
Xaa Leu Gly Pro
        115
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

```
Met Pro Asp Asn Leu His Leu His Thr Leu Leu Xaa Lys Phe Leu Gln
1               5                   10                  15
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
            20                  25                  30
Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
        35                  40                  45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Xaa Cys Tyr Leu
    50                  55                  60
Ile Gly Xaa Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg
65                  70                  75                  80
Ala Phe
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

```
Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1               5                   10                  15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
```

```
            20                  25                  30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
        35                  40                  45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
    50                  55                  60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
65                  70                  75                  80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
                85                  90                  95
Leu Lys Ser Phe Leu Glu Lys Ala Xaa Arg Gln Arg Ala Val Leu Arg
            100                 105                 110
His Phe Cys Ala
        115
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

```
Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
1               5                   10                  15
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
            20                  25                  30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
        35                  40                  45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr
    50                  55                  60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro
65                  70                  75                  80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr
                85                  90                  95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu
            100                 105                 110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu
        115                 120                 125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln
    130                 135                 140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile
145                 150                 155                 160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile
                165                 170                 175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile
            180                 185                 190
Ile Leu Lys Ala Cys Ala
        195
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

```
Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln
1               5                  10                  15
Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
            20                  25                  30
Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
        35                  40                  45
Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
    50                  55                  60
Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
65                  70                  75                  80
Ala Arg Gly His Val
                85
```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

```
Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe
1               5                  10                  15
Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile
            20                  25                  30
Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg
        35                  40                  45
Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp
    50                  55                  60
Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val
65                  70                  75                  80
Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr
                85                  90                  95
Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe
            100                 105                 110
Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro
        115                 120                 125
Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu
    130                 135                 140
Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro
145                 150                 155                 160
Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp
                165                 170                 175
Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu
            180                 185                 190
```

```
Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly
        195                 200                 205
Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu
    210                 215                 220
Gly Leu Ile Glu Tyr Ser Asn Asn Asn Asn Pro Arg Lys Lys Ile Tyr
225                 230                 235                 240
Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys
                245                 250                 255
Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu
            260                 265                 270
Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp
        275                 280                 285
Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln
    290                 295                 300
Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
305                 310                 315                 320
Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
                325                 330                 335
Phe Tyr Asp Phe Leu Val Phe
            340
```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

```
Met Thr Ser Val Val Ile Lys Pro His Ala Tyr Gly Glu Gln Val Gln
1               5                   10                  15
Glu Ile Glu Glu Glu Ser Asp Ser Asp Tyr Glu Lys Asn Asn Asp Gln
            20                  25                  30
Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln
        35                  40                  45
Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr
    50                  55                  60
His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu
65                  70                  75                  80
Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His
                85                  90                  95
Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg
            100                 105                 110
Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp
        115                 120                 125
Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser
    130                 135                 140
His Tyr Ala Glu Phe Leu Arg Thr Gln Xaa Pro His Phe Lys Ile Gln
145                 150                 155                 160
Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Xaa Trp Xaa
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

```
Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1               5                  10                  15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
            20                  25                  30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
        35                  40                  45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
    50                  55                  60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65                  70                  75                  80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
                85                  90                  95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
            100                 105                 110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
        115                 120                 125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
    130                 135                 140
Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145                 150                 155                 160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
                165                 170                 175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
            180                 185                 190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
        195                 200                 205
Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr
    210                 215                 220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
225                 230                 235                 240
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
                245                 250                 255
Ala Lys Lys Asn
            260
```

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

```
Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
1               5                  10                  15
Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
            20                  25                  30
Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
        35                  40                  45
Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
    50                  55                  60
Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
65                  70                  75                  80
Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
                85                  90                  95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
            100                 105                 110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
        115                 120                 125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Xaa Phe Gly Ile
    130                 135                 140
Gly
145
```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

```
Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1               5                  10                  15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
            20                  25                  30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
        35                  40                  45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
    50                  55                  60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65                  70                  75                  80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
                85                  90                  95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
            100                 105                 110
Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
        115                 120                 125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
    130                 135                 140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145                 150                 155                 160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
                165                 170                 175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
            180                 185                 190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
        195                 200                 205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
```

```
    210                 215                 220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225                 230                 235                 240
Val Phe Leu Ser Gly Val Lys Asn
                245
```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

```
Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1               5                  10                  15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
            20                  25                  30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
        35                  40                  45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
    50                  55                  60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65                  70                  75                  80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
                85                  90                  95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
            100                 105                 110
Leu Leu Trp Trp Phe Xaa Leu
        115
```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

```
Val Asn Leu Met Asp Tyr Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu
1               5                  10                  15
Asn Thr Gln Arg Leu Ile Val Ser Asn Lys Leu Ala Ile Asp Val Gln
            20                  25                  30
Tyr Gly Met Leu Gln Ser Val Arg Lys Asn Tyr Pro Asp Val Val Asp
        35                  40                  45
```

```
Gly Gly Val Arg Glu Gly Pro Phe Trp Val Leu Ala Gly Ala Leu Met
    50                  55                  60
Pro Ser Ile Leu Ile Glu Ile Gly Tyr Asn Ser His Ala Ile Glu Ser
65                  70                  75                  80
Lys Arg Ile Gln Ser Lys Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile
                85                  90                  95
Ala Asp Gly Ile Asp Ser Phe Phe Ser Lys Asn Asp
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

```
Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
1               5                   10                  15
Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
            20                  25                  30
Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
        35                  40                  45
Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
    50                  55                  60
Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
65                  70                  75                  80
Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
                85                  90                  95
Tyr Leu Gln Glu Lys Xaa Xaa Ile Phe Pro Thr Xaa Lys Xaa Xaa Xaa
            100                 105                 110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
        115                 120                 125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
    130                 135                 140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

```
Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1               5                  10                  15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
            20                  25                  30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
        35                  40                  45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
    50                  55                  60
Val Gly Val Thr Leu Leu Ala Leu Ala Asn Ser Xaa Arg Thr Met Arg
65                  70                  75                  80
Ala
```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

```
Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1               5                  10                  15
Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile
            20                  25                  30
Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile
        35                  40                  45
Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys
    50                  55                  60
Glu Ile Leu Met Thr Val Leu Ala Leu Lys Xaa Val Pro Met Gln Xaa
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

```
Leu Ala Gly Leu Xaa Val Gly Cys Xaa Arg Met Lys Gln Thr Phe Trp
1               5                  10                  15
Xaa Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
            20                  25                  30
```

```
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
        35                  40                  45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
    50                  55                  60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
65                  70                  75                  80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
                85                  90                  95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
            100                 105                 110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
        115                 120                 125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
    130                 135                 140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
145                 150                 155                 160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
                165                 170                 175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
            180                 185                 190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
        195                 200                 205
Thr Cys Xaa Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr
    210                 215                 220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr
225                 230                 235                 240
Thr Phe Ser Xaa Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr
                245                 250                 255
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys
            260                 265                 270
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe
        275                 280                 285
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr
    290                 295                 300
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly
305                 310                 315                 320
Thr Phe Thr Phe Asn
                325
```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

```
Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser
1               5                   10                  15
Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser
            20                  25                  30
Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala
        35                  40                  45
Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn
    50                  55                  60
Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly
65                  70                  75                  80
```

```
Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys
                85                  90                  95
Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe
            100                 105                 110
Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn
        115                 120                 125
Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu
    130                 135                 140
Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile
145                 150                 155                 160
Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser
                165                 170                 175
Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly
            180                 185                 190
Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly
        195                 200                 205
Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg
    210                 215                 220
Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr
225                 230                 235                 240
Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile
                245                 250                 255
Gln Thr Ala Asp Ala Met Leu Gln Thr Val Asn Ser Leu Lys Arg
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

```
Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe
1               5                   10                  15
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn
            20                  25                  30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr
        35                  40                  45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser
    50                  55                  60
Ala Lys Tyr Leu Asn Arg Xaa Leu Asn Arg Val Pro Ile Leu Ser Xaa
65                  70                  75                  80
Ile Tyr Thr Xaa Arg Xaa Leu Gly Xaa Val
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

```
Val Gly Ala Met Pro Thr Ile Gln Ile Arg Xaa Phe Gly Ala Gly Gly
1               5                  10                  15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
            20                  25                  30
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
        35                  40                  45
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
    50                  55                  60
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65                  70                  75                  80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Xaa Thr Tyr
                85                  90                  95
Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Xaa Asp Lys Thr
            100                 105                 110
Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
        115                 120                 125
Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
    130                 135                 140
Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145                 150                 155                 160
Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
                165                 170                 175
Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Xaa
            180                 185                 190
Gln Pro Gly
        195
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

```
Met Arg Xaa Glu Lys Ile Met Thr Asn Phe Glu Lys Xaa Ile Ala Gln
1               5                  10                  15
Asn Arg Leu Lys Thr Asn Ala Val Leu Thr Thr Tyr Cys Ala Ile Phe
            20                  25                  30
Ala Phe Ile Gly Leu Leu Val Asp Ala Ile Arg Ile Asn Ala Asn Asp
        35                  40                  45
Leu Gly Ile Ala Leu Phe Lys Leu Met Thr Phe Gln Ile Phe Pro Thr
    50                  55                  60
Xaa Thr Ile Val Met Phe Val Val Ala Phe Val Ile Xaa Xaa Ser Leu
65                  70                  75                  80
Tyr Pro Lys Phe
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

```
Met Xaa Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1               5                  10                  15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
            20                  25                  30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
        35                  40                  45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Xaa Pro Val Gly
    50                  55                  60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

```
Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1               5                  10                  15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
            20                  25                  30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
        35                  40                  45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
    50                  55                  60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65                  70                  75                  80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
                85                  90                  95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
            100                 105                 110
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
        115                 120                 125
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
    130                 135                 140
```

```
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145                 150                 155                 160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
                165                 170                 175
Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Xaa Ala Xaa Ala Arg Asp
            180                 185                 190
Arg Leu Xaa Xaa
        195
```

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

```
Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1               5                   10                  15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
            20                  25                  30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
        35                  40                  45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
    50                  55                  60
Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
65                  70                  75                  80
Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
                85                  90                  95
Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
            100                 105                 110
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
        115                 120                 125
Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
    130                 135                 140
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
145                 150                 155                 160
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
                165                 170                 175
Leu Val Lys
```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

```
Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1               5                  10                  15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
            20                  25                  30
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp
        35                  40                  45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
    50                  55                  60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
65                  70                  75                  80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
                85                  90                  95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
            100                 105                 110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
        115                 120                 125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
    130                 135                 140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
145                 150                 155                 160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
                165                 170                 175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
            180                 185                 190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
        195                 200                 205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
    210                 215                 220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
225                 230                 235                 240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Xaa Ile Ala Ile Glu
                245                 250                 255
Xaa Ser Glu Leu Xaa Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly
            260                 265                 270
Tyr Gly Ser Gln Lys Xaa Ile Trp Thr Tyr Thr Xaa Gly Val
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

```
Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly
1               5                  10                  15
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe
            20                  25                  30
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser
        35                  40                  45
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Xaa Ile Arg
```

```
    50                  55                  60
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln
65                  70                  75                  80
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu
                85                  90                  95
Ile Ser Arg Tyr Lys Asp Val Ser Ile Xaa Leu Xaa Asp Thr
            100                 105                 110
```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

```
Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1               5                   10                  15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
            20                  25                  30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
        35                  40                  45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
    50                  55                  60
Asp Leu Thr Met Glu Phe Ile Xaa Val Gly Ala Ile Ser Gly Ala Met
65                  70                  75                  80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
                85                  90                  95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
            100                 105                 110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

```
Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1               5                   10                  15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
            20                  25                  30
```

```
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
        35                  40                  45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
    50                  55                  60
Val Asp Ala Ile Gly Leu Pro Ala Pro Xaa Lys Arg Glu Arg Lys Arg
65                  70                  75                  80
Ser Tyr Cys Cys Gln Thr His Gln Ile Arg Asp Ala Pro Phe Arg
                85                  90                  95
```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

```
Leu Pro Ile Ile Leu Xaa Val Ile Val Met Met Phe Phe Ser Lys Ile
1               5                   10                  15
Val Gly Asp Phe Ile Glu Lys His Tyr Arg Val Lys Thr Leu Ala Phe
            20                  25                  30
Val Phe Leu Leu Val Val Gly Val Phe Leu Phe Leu Glu Gly Leu His
        35                  40                  45
Leu His Ile Asn Lys Asn Tyr Leu Tyr Ala Gly Ile Gly Phe Ala Leu
    50                  55                  60
Leu Ile Glu Cys Leu Xaa Ile Phe Ile Glu Lys Lys Met Lys Lys Ser
65                  70                  75                  80
```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

```
Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1               5                   10                  15
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
            20                  25                  30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
        35                  40                  45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
    50                  55                  60
Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
```

```
65                  70                  75                  80
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
                85                  90                  95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
            100                 105                 110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
        115                 120                 125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
    130                 135                 140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
145                 150                 155                 160
Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
                165                 170                 175
Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
            180                 185                 190
Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
        195                 200                 205
Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
    210                 215                 220
Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
225                 230                 235                 240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
                245                 250                 255
Leu Asp Phe Ile Gln Asn Lys Lys Phe
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

```
Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr
1               5                   10                  15
Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu
            20                  25                  30
Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys
        35                  40                  45
Ala Xaa Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro
    50                  55                  60
```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

```
Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys
1               5                  10                  15
Ser Met Ser Asp Ser Glu Ile Phe Ala Xaa Xaa Cys Val Gly Met Ala
            20                  25                  30
Ser Val Xaa Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro
        35                  40                  45
Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu
    50                  55                  60
Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
65                  70                  75                  80
Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Xaa Ala
                85                  90                  95
Xaa Gly Ala Ser Thr Gly Xaa His Leu Ala Leu His Val Gly Ala Met
            100                 105                 110
Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
        115                 120                 125
Val Val Gly Gly Phe Leu Gly Met Glu His
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

```
Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1               5                  10                  15
Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
            20                  25                  30
Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
        35                  40                  45
Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
    50                  55                  60
His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65                  70                  75                  80
Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
                85                  90                  95
Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
            100                 105                 110
Ala Ile Ile Xaa
        115
```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

```
Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Xaa
1               5                  10                  15
Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
            20                  25                  30
Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
        35                  40                  45
Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
    50                  55                  60
Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
65                  70                  75                  80
Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
                85                  90                  95
Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
            100                 105                 110
Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
        115                 120                 125
Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
    130                 135                 140
Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
145                 150                 155                 160
Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
                165                 170                 175
Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
            180                 185                 190
Xaa Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Xaa
        195                 200                 205
Phe Lys Asn Xaa Xaa Ala Leu Thr Pro Xaa Asp Leu Ile Glu Lys Xaa
    210                 215                 220
Lys Arg Leu
225
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

```
Val Xaa Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1               5                  10                  15
Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
            20                  25                  30
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
```

```
        35                  40                  45
Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
    50                  55                  60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
65                  70                  75                  80
Pro Lys Asp Leu Xaa Gln Ala Lys Met Gln Phe Xaa Met Leu Gln Asn
                85                  90                  95
Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

```
Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser
1               5                   10                  15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe
            20                  25                  30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala
        35                  40                  45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala
    50                  55                  60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp
65                  70                  75                  80
Glu Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Xaa Asn Ile
                85                  90                  95
Cys
```

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

```
Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val
1               5                   10                  15
Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys
            20                  25                  30
```

```
Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr
        35                  40                  45
Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys
    50                  55                  60
Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala
65                  70                  75                  80
Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln
                85                  90                  95
Gly Phe Lys Ser Ile Ile Pro Asn Lys Lys Ile Tyr Phe Glu Phe Leu
            100                 105                 110
Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly
        115                 120                 125
Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro
    130                 135                 140
Ser
145
```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

```
Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val
1               5                   10                  15
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr
            20                  25                  30
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr
        35                  40                  45
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala
    50                  55                  60
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr
65                  70                  75                  80
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys
                85                  90                  95
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe
            100                 105                 110
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln
        115                 120                 125
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val
    130                 135                 140
Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe
145                 150                 155                 160
Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser
                165                 170                 175
Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp
            180                 185                 190
Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn
        195                 200                 205
Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala
    210                 215                 220
Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu
225                 230                 235                 240
Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr
                245                 250                 255
```

```
Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr
            260                 265                 270
Phe
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

```
Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1               5                  10                  15
Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
            20                  25                  30
Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
        35                  40                  45
Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
    50                  55                  60
Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
65                  70                  75                  80
Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
                85                  90                  95
Ser Val Val Thr Ile Ala Glu Xaa Phe Arg Ile Ala Gln Gln Lys Xaa
            100                 105                 110
Asn Val Ser Tyr Asp Phe Xaa Pro Ile Tyr Leu Glu Xaa Ala Leu Ile
        115                 120                 125
Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
    130                 135                 140
Lys Ile Leu Asn
145
```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

```
Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1               5                  10                  15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
```

```
            20                  25                  30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
        35                  40                  45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
    50                  55                  60
Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr
65                  70                  75                  80
Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu
                85                  90                  95
Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu
            100                 105                 110
Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Xaa Lys Gln
        115                 120                 125
Val Asn Leu Phe Lys Thr
    130
```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

```
Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile
1               5                   10                  15
Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val
            20                  25                  30
Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly
        35                  40                  45
Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
    50                  55                  60
Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Xaa
65                  70                  75                  80
Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
                85                  90                  95
Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
            100                 105                 110
Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
        115                 120                 125
Leu Ile Thr Ser Pro
    130
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

```
Met Pro Pro Thr Xaa Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1               5                  10                  15
Asn Pro Leu Xaa Xaa Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
            20                  25                  30
Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
        35                  40                  45
Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
    50                  55                  60
Ile Arg Ser Leu Leu Lys Pro
65                  70
```

(2) INFORMATION FOR SEQ ID NO.202.

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

```
Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1               5                  10                  15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
            20                  25                  30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
        35                  40                  45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
    50                  55                  60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
65                  70                  75                  80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
                85                  90                  95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
            100                 105                 110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
        115                 120                 125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
    130                 135                 140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
145                 150                 155                 160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
                165                 170                 175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
            180                 185                 190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
        195                 200                 205
Asn His Asn Gln Phe Phe Ile Lys Asn
    210                 215
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

```
Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe
1               5                  10                  15
Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu
            20                  25                  30
Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg
        35                  40                  45
Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu
    50                  55                  60
Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

```
Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1               5                  10                  15
Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
            20                  25                  30
Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys
        35                  40                  45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
    50                  55                  60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65                  70                  75                  80
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
                85                  90                  95
Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
            100                 105                 110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
        115                 120                 125
Thr Ala Leu Asn Glu Asn Met Thr Xaa Pro Ile His Ser Leu Lys Ser
    130                 135                 140
Ile Thr Arg Ser Xaa Pro Tyr Tyr Lys Glu Val Asn Xaa Xaa Lys Ile
145                 150                 155                 160
Tyr Xaa Xaa Xaa Ile Thr Leu Pro Leu Xaa Xaa Lys Asn Xaa Asn Xaa
```

```
                165                 170                 175
Ile Xaa Xaa Leu Asn Phe Xaa Leu Asn Ile Asp Xaa Phe Leu Tyr Xaa
            180                 185                 190
```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

```
Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1               5                  10                  15
Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp
            20                  25                  30
Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys
        35                  40                  45
Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu
    50                  55                  60
Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu
65                  70                  75                  80
Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys
                85                  90                  95
Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu Gln Asn Met
            100                 105                 110
Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu
        115                 120                 125
Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu
    130                 135                 140
Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly
145                 150                 155                 160
Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala
                165                 170                 175
Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu
            180                 185                 190
Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr
        195                 200                 205
Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr
    210                 215                 220
Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln
225                 230                 235                 240
Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

```
Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile
1               5                  10                  15
Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys
            20                  25                  30
Ala Ile Ala His Ser Val Gly Xaa Ile Leu Arg Trp Tyr Val Ser Gly
        35                  40                  45
His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp
    50                  55                  60
Ala Ser Val Ile Ala Gly Phe Val Leu Arg Xaa Lys Leu Ala Leu Ser
65                  70                  75                  80
Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly
                85                  90                  95
Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr
            100                 105                 110
Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu
        115                 120                 125
Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu
    130                 135                 140
Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser
145                 150                 155                 160
Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala
                165                 170                 175
Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr
            180                 185                 190
Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val
        195                 200                 205
Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro
    210                 215                 220
Phe Ile Leu Ala Ser Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met
225                 230                 235                 240
Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys
                245                 250                 255
Arg Arg Xaa Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser
            260                 265                 270
Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser
        275                 280                 285
Leu Pro Lys Leu Val
    290
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

```
Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
1               5                  10                  15
```

```
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
            20                  25                  30
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
        35                  40                  45
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
    50                  55                  60
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro
65                  70                  75                  80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
                85                  90                  95
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
            100                 105                 110
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
        115                 120                 125
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

```
Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1               5                   10                  15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
            20                  25                  30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
        35                  40                  45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
    50                  55                  60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Xaa Gln His Leu Arg
65                  70                  75                  80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
                85                  90                  95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
            100                 105                 110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
        115                 120                 125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

```
Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe
1               5                  10                  15
Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys
            20                  25                  30
Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys
        35                  40                  45
Pro Ile Asn Xaa Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr
    50                  55                  60
Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
65                  70                  75                  80
Arg Tyr Gly
```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

```
Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
1               5                  10                  15
Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
            20                  25                  30
Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
        35                  40                  45
Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
    50                  55                  60
Ala Lys Glu Lys His Val Lys Glu Asn Val Xaa Pro Leu His Phe Cys
65                  70                  75                  80
Xaa Ala Gly His Ile Xaa Val Val Pro Pro Gly Xaa Xaa Xaa Xaa Xaa
                85                  90                  95
Asp Ser Phe Xaa Xaa Ile Ile Lys Glu Gly Phe Leu Tyr Gly Arg Gly
            100                 105                 110
Ala Gln Asp Met Lys Gly Gly Val Gly Xaa Phe Xaa Arg Cys Xaa Xaa
        115                 120                 125
Lys Phe
    130
```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

```
Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
1               5                  10                  15
Thr Arg Ile Glu Asp Ala Lys Leu Ile Ala His Phe Lys Ile Ser Gln
            20                  25                  30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Ile Ala Ser
        35                  40                  45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Val Lys Ile
    50                  55                  60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
65                  70                  75                  80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
                85                  90                  95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu
            100                 105                 110
Arg Gly His Val Tyr Ser Leu Phe Ile Asn Glu Lys Gln Thr Arg Met
        115                 120                 125
Pro Leu Ser Val Leu Leu Val Ser Gly Gly His Ser Leu Ile Leu Glu
    130                 135                 140
Ala Arg Asp Tyr Glu Asp Ile Lys Ile Val Ala Thr Ser Leu Asp Asp
145                 150                 155                 160
Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
                165                 170                 175
Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
            180                 185                 190
Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
        195                 200                 205
Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
    210                 215                 220
Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
225                 230                 235                 240
Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
                245                 250                 255
Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
            260                 265                 270
Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
        275                 280                 285
Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
    290                 295                 300
Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
305                 310                 315                 320
Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
                325                 330                 335
Lys Asn Phe Glu
            340
```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

```
Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu
1               5                  10                  15
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu
            20                  25                  30
Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr
        35                  40                  45
Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg
    50                  55                  60
Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu
65                  70                  75                  80
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys
                85                  90                  95
Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Xaa Xaa
            100                 105                 110
Lys Thr Xaa Xaa Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser
        115                 120                 125
Thr Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp
    130                 135                 140
Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile
145                 150                 155                 160
Leu Asn Met Ala Gly Leu Lys Trp
                165
```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

```
Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe
1               5                  10                  15
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile
            20                  25                  30
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val
        35                  40                  45
Arg Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile
    50                  55                  60
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu
65                  70                  75                  80
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln
                85                  90                  95
Xaa His Ser Ser Xaa Xaa Lys Leu Val Xaa Ala Arg Ser Asn Asp Glu
            100                 105                 110
Leu Gly Arg Xaa Gln Thr Xaa Asp Xaa
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

```
Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1               5                  10                  15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
            20                  25                  30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
        35                  40                  45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
    50                  55                  60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65                  70                  75                  80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
                85                  90                  95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
            100                 105                 110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
        115                 120                 125
Xaa Gly Ala Xaa Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile
    130                 135                 140
Leu Val Ala Leu Gly
145
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

```
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1               5                  10                  15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
            20                  25                  30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
        35                  40                  45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
    50                  55                  60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65                  70                  75                  80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
```

```
                85                  90                  95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
            100                 105                 110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
        115                 120                 125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
    130                 135                 140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145                 150                 155                 160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
                165                 170                 175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
            180                 185                 190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
        195                 200                 205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
    210                 215                 220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225                 230                 235                 240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
                245                 250                 255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
            260                 265                 270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
        275                 280                 285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
    290                 295                 300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305                 310                 315                 320
Gly Gly Phe His Phe
                325
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

```
Leu Arg Ser Ile Ser Arg Ile Lys Met Leu Ser Val Tyr Glu Lys Gly
1               5                   10                  15
Asn Ala Leu Asp Lys Arg Val Leu Glu Glu Trp Leu Leu Ser Glu Asp
            20                  25                  30
Ile Leu Met Glu Asn Ala Ala Met Ala Leu Glu Arg Ala Val Leu Gln
        35                  40                  45
Asn Ala Ser Leu Gly Ala Lys Val Ile Ile Leu Cys Gly Ser Gly Asp
    50                  55                  60
Asn Gly Gly Asp Gly Tyr Thr Leu Ala Arg Arg Leu Val Gly Arg Phe
65                  70                  75                  80
Lys Thr Leu Val Phe Glu Met Lys Leu Ala Lys Ser Pro Met Cys Gln
                85                  90                  95
Leu Gln Lys Glu Arg Ala Lys Lys Val Gly Val Val Ile Lys Ala Trp
            100                 105                 110
Glu Glu Lys Asn Glu Asp Leu Glu Cys Asp Val Leu Val Asp Cys Val
        115                 120                 125
Val Gly Ser Ala Phe Lys Gly Gly Leu Glu Pro Phe Leu Asp Phe Glu
```

```
    130                 135                 140
Ser Leu Ser Gln Lys Ala Arg Phe Lys Ile Ala Cys Asp Ile Pro Ser
145                 150                 155                 160
Gly Ile Asp Ser Lys Gly Arg Val Asp Lys Arg Ala Phe Lys Xaa Gly
                165                 170                 175
Tyr Arg Leu Ser Ala Trp Ala Leu Phe Lys Ser Cys Leu Leu Ser Xaa
            180                 185                 190
Lys Xaa Lys Xaa Tyr Ile Xaa Xaa Leu Lys Xaa Xaa His Leu Xaa Val
        195                 200                 205
Phe Asn Gln Ile Tyr Glu Ile Pro Thr Xaa Thr Phe Leu Leu Glu Lys
    210                 215                 220
Xaa Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
225                 230                 235                 240
Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

```
Met Ala Leu Asp Lys Arg Ile Trp Met His Phe Asp Leu Leu Pro Phe
1                   5                   10                  15
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu
            20                  25                  30
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly
        35                  40                  45
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
    50                  55                  60
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
65                  70                  75                  80
Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
                85                  90                  95
Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
            100                 105                 110
Arg Xaa Ser Phe Ile Val Gly Ala Phe Xaa Xaa Asn Xaa Pro Asp Xaa
        115                 120                 125
Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

```
Val Leu Met Ala Leu Xaa Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
1               5                  10                  15
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
            20                  25                  30
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
        35                  40                  45
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
    50                  55                  60
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
65                  70                  75                  80
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
                85                  90                  95
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
            100                 105                 110
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
        115                 120                 125
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
    130                 135                 140
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
145                 150                 155                 160
Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
                165                 170                 175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
            180                 185                 190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
        195                 200                 205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
    210                 215                 220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
225                 230                 235                 240
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
                245                 250                 255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
            260                 265                 270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
        275                 280                 285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
    290                 295                 300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
305                 310                 315                 320
Ser Leu Leu Pro Trp Arg
                325
```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

```
Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe
1               5                  10                  15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr
            20                  25                  30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His
        35                  40                  45
Val Val Phe Gly Thr Gly Arg Arg Gln Glu Asn Leu Gln Lys Leu Gln
    50                  55                  60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn
65                  70                  75                  80
Lys Pro Glu Thr Lys Arg Ala Ile Glu Thr Ile Phe Ser Met Thr Asp
                85                  90                  95
Arg Ile Asp Ala Leu Ile Asn Asn Ala Gly Leu Ala Leu Gly Leu Asn
            100                 105                 110
Lys Ala Tyr Glu Cys Glu Leu Asp Asp Trp Glu Val Met Ile Asp Thr
        115                 120                 125
Asn Ile Lys Gly Leu Leu His Leu Thr Arg Leu Ile Leu Pro Ser Met
    130                 135                 140
Ile Glu His Asp Gln Gly Thr Ile Ile Asn Leu Gly Ser Ile Ala Gly
145                 150                 155                 160
Thr Tyr Ala Tyr Pro Gly Gly Xaa Val Tyr Gly Ala Ser Lys Ala Xaa
                165                 170                 175
Val Lys Gln Xaa Ser Xaa Asn Leu Arg Ala Asp Val Ala Gly Thr Asn
            180                 185                 190
Thr Arg Gly Arg Arg Trp Asn Pro Gly Cys Val Ala Lys Pro Lys Val
        195                 200                 205
Ser Arg Val Arg Gly Lys Gly Asp Lys Pro Lys Pro Lys Ser Gly Tyr
    210                 215                 220
Glu Lys His Pro Leu Pro Gln Thr Thr Arg Gln Gly Leu Thr Ser Gly
225                 230                 235                 240
```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

```
Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1               5                  10                  15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
            20                  25                  30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
        35                  40                  45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
    50                  55                  60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
65                  70                  75                  80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
                85                  90                  95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
            100                 105                 110
Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu
        115                 120                 125
Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr
    130                 135                 140
```

```
Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys
145                 150                 155                 160
Arg Ile Ala Leu Gly Xaa Gly Leu Glu Xaa Xaa Glu Ile Asn Arg Ile
                165                 170                 175
Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn
            180                 185                 190
Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Xaa Xaa
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

```
Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1               5                   10                  15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
            20                  25                  30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
        35                  40                  45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
    50                  55                  60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65                  70                  75                  80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
                85                  90
```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

```
Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1               5                   10                  15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
            20                  25                  30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
        35                  40                  45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
```

```
    50                  55                  60
Leu Xaa Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Xaa Leu
65                  70                  75                  80
Ser Xaa
```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

```
Leu Ser Leu Met Xaa Val Leu Asn Ala Lys Glu Cys Val Xaa Pro Ile
1               5                  10                  15
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
            20                  25                  30
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
        35                  40                  45
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
    50                  55                  60
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65                  70                  75                  80
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
                85                  90                  95
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
            100                 105                 110
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
        115                 120                 125
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
    130                 135                 140
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145                 150                 155                 160
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
                165                 170                 175
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
            180                 185                 190
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
        195                 200                 205
Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
    210                 215                 220
Pro Ile Lys Ala Trp Gln Asn Lys Lys
225                 230
```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

```
Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
1               5                  10                  15
His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
            20                  25                  30
Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
        35                  40                  45
Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
    50                  55                  60
Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
65                  70                  75                  80
Cys Ile Ser Ser Leu
                85
```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

```
Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Xaa Ala Met Lys Arg
1               5                  10                  15
Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
            20                  25                  30
Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
        35                  40                  45
Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
    50                  55                  60
Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
65                  70                  75                  80
Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
                85                  90                  95
Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
            100                 105                 110
Arg Glu Phe
        115
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

```
Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
1               5                  10                  15
Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu
            20                  25                  30
Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile
        35                  40                  45
Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn
    50                  55                  60
Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg
65                  70                  75                  80
Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu
                85                  90                  95
Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly
            100                 105                 110
Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr
        115                 120                 125
Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Xaa Pro Asp Val Met
    130                 135                 140
Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro
145                 150                 155                 160
Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr
                165                 170                 175
Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly
            180                 185                 190
Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln
        195                 200                 205
Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala
    210                 215                 220
Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn
225                 230                 235                 240
Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu
                245                 250                 255
Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala
            260                 265                 270
Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe
        275                 280                 285
Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr
    290                 295                 300
Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn
305                 310                 315                 320
Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys
                325                 330                 335
Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
            340                 345                 350
Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
        355                 360                 365
Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu
    370                 375                 380
Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn
385                 390
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

```
Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1               5                  10                  15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
            20                  25                  30
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
        35                  40                  45
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
    50                  55                  60
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65                  70                  75                  80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
                85                  90                  95
Xaa Phe Lys Arg Cys Lys
            100
```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

```
Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Xaa Phe Leu Asn Thr Gln
1               5                  10                  15
Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
            20                  25                  30
Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
        35                  40                  45
Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
    50                  55                  60
Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
65                  70                  75                  80
Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
                85                  90                  95
Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
            100                 105                 110
Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
        115                 120                 125
Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
    130                 135                 140
Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
145                 150                 155                 160
Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr
                165                 170                 175
Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu
```

```
            180                 185                 190
Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp
        195                 200                 205
Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser
    210                 215                 220
Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val
225                 230                 235                 240
Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys
                245                 250                 255
Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys
            260                 265                 270
Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu
        275                 280                 285
Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp
    290                 295                 300
Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser
305                 310                 315                 320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp
                325                 330                 335
Xaa Lys Xaa Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr
            340                 345                 350
Lys Thr Gln Xaa Arg Met Ile Xaa Gly Cys Xaa
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATATCCATGG TGAGTTTGAT GA 22

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGAATTCAA TTTTTTATTT TGCCA 25

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

AATTCCATGG TGGGGGCTAT G 21

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGAATTCTC GATAGCCAAA ATC 23

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

ATTTCCATGG TCATGTCTCA TATT 24

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

ATGAATTCCA TCTTTTATTC CAC 23

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

AACCATGGTG ATTTTAAGCA TTGAAAG 27

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

AAGAATTCCA CTCAAAATTT TTTAACAG 28

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

GATCATCCAT ATGTTATCTT CTAAT 25

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

TGAATTCAAC CATTTTAACC CTG 23

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

TATACCATGG TGAAATTTTT TCTTTTA 27

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

AGAATTCAAT TGCGTCTTGT AAAAG 25

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

TTATGGATCC AAACCAATTA AAACT 25

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

TATCTCGAGT TATAGAGAAG GGC 23

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

ATATCCATGG TGAGTTTGAT GA 22

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGAATTCAA TTTTTTATTT TGCCA 25

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

AATTCCATGG CTATCCAAAT CCG 23

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ATGAATTCGC CAAAATCGTA GTATT 25

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

GATACCATGG AATTTATGAA AAAG 24

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

TGAATTCGAA AAAGTGTAGT TATAC 25

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

TTGAACACTT TTGATTATGC GG 22

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

GGATTATGCG ATTGTTTTAC AAG 23

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

GTCTTTAGCA AAAATGGCGT C 21

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

AATGAGCGTA AGAGAGCCTT C 21

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

CTTATGGGGG TATTGTCA 18

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

AGCATGTGGG TATCCAGC 18

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

AGGTTGTTGC CTAAAGACT 19

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

CTGCCTCCAC CTTTGATC 18

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

ACCAATATCA ATTGGCACT 19

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ACTTGGAAAA GCTCTGCA 18

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

CTTGCTTGTC ATATCTAGC 19

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

GTTGAAGTGT TGGTGCTA 18

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

CAAGCAAGTG GTTTGGTTTT AG 22

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

TGGAAAGAGC AAATCATTGA AG 22

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

GCCCATAATC AAAAAGCCCA T 21

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

CTAAAACCAA ACCACTTGCT TGTC 24

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

GTAAAACGAC GGCCAG 16

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

CAGGAAACAG CTATGAC 17

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

ATCTTACCTA TCACCTCAAA T 21

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

AGACAGCAAC ATCTTTGTGA A 21

CLAIMS

1. A substantially pure nucleic acid encoding an *H. pylori* polypeptide, said nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-114.

2. A substantially pure nucleic acid from naturally occurring *H. pylori* which hybridizes under stringent conditions to a nucleic acid which encodes an *H. pylori* polypeptide, said nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-114.

3. A method of evaluating a compound for the ability to bind an *H. pylori* nucleic acid comprising: contacting said compound with an *H. pylori* nucleic acid selected from the group consisting of SEQ ID NO:1-114 and determining if said compound binds said *H. pylori* nucleic acid.

4. The method of claim 3, wherein said compound is an activator of the bacterial life cycle.

5. The method of claim 3, wherein said compound is an inhibitor of the bacterial life cycle.

6. The method of claim 3, wherein said method is performed *in vitro*.

7. The method of claim 3, wherein said method is performed *in vivo*.

8. A method of generating a vaccine for immunizing a subject against *H. pylori* infection comprising: immunizing said subject with a nucleic acid encoding an *H. pylori* polypeptide or a fragment thereof, said nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-114, and a therapeutically acceptable carrier.

9. A method of detecting the presence of a *Helicobacter* species in a sample comprising:

contacting said sample with a nucleic acid encoding an *H. pylori* polypeptide, said nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-114;

hybridizing said sample to said nucleic acid;

said hybridization being indicative of the presence of said *Helicobacter* species in said sample.

10. The method of claim 9, wherein said *Helicobacter* species is *H. pylori*.

11. The method of claim 9, wherein said nucleic acid is 20 or more nucleotides in length.

12. A method of inhibiting expression of a gene from a *Helicobacter* species comprising: administering to said species an *H. pylori* antisense nucleic acid selected from the group consisting of SEQ ID NO:1-114.

13. The method of claim 12, wherein said *Helicobacter* species is *H. pylori*.

14. The method of claim 12, wherein said antisense nucleic acid is administered in a carrier.

15. The method of claim 12, wherein said carrier is a liposome or a bacteriophage.

16. The method of claim 12, wherein said antisense nucleic acid is 20 or more nucleotides in length.

17. The method of claim 12, wherein said antisense nucleic acid is capable of binding to *Helicobacter* nucleic acid or mRNA.

18. A method of generating a vaccine for immunizing a subject against *H. pylori* infection comprising: immunizing said subject with a nucleic acid encoding an *H. pylori* polypeptide or a fragment thereof, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:115-228, and a therapeutically acceptable carrier.

Sequence Identifer	Sequence Name	BLAST hit	Description
1,	3987580,		
2,	55843,		
3,	1365943,		
4,	914087,		
5,	23438887,		
6,	24409641,		
7,	26258562,	sp|P20021|CADA_STAAV. (HPP 296)	probable cadmium-transporting ATPase,
8,	5138,		
9,	21647676,	. (HPP 149)	mature-parasite-infected erythrocyte surface antigen,
10,	207817,		
11,	116018,		
12,	486075,		
13,	30708287,		
14,	6828218,		
15,	24089087,		
16,	35163962,		
17,	6288949,	. (HPP 523)	flagellar biosynthetic protein,
18,	35345228,	. (HPP 4061)	norepinephrine transporter,
19,	24406567,	sp|P10408|SECA_ECOLI. (HPP 243)	Protein secretion secA subunit,
20,	24409577,		
21,	15126875,		
22,	25595387,		
23,	5869090,		
24,	23912807,	sp|P26276|ALGC_PSEAE. (HPP 214)	phosphomannomutase,
25,	598933,		
26,	24500088,		
27,	4882842,		
28,	4062813,		
29,	35269000,		
30,	23535937,	sp|Q03523|MURE_BACSU. (HPP 194)	UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE,
31,	2042312,		
32,	30478562,		
33,	34161500,	sp|P31548|YABJ_ECOLI. (HPP 372)	HYPOTHETICAL ABC TRANSPORTER,
34,	33203192,		
35,	12505125,	sp|P18783|EXBB_ECOLI. (HPP 161)	biopolymer transport exbB protein,
36,	22379952,	sp|P31547|YAEE_ECOLI. (HPP 495)	HYPOTHETICAL 23.3 KD PROTEIN-INTEGRAL MEMBRANE,
37,	489057,		
38,	5312712,		
39,	24220627,	gi|311022|gp|L08012|. (HPP 230)	major surface LPS-antigen,
40,	12698442,		
41,	4338438,	sp|P31219|YBBA_ECOLI. (HPP 455)	hypothetical abc transporter n tesA region,
42,	2149041,		
43,	4569693,	(HPP 463)	Cell division inhibitor,
44,	3179505,	sp|P33916|YEJF_ECOLI. (HPP 348)	HYPOTHETICAL ABC TRANSPORTER,
45,	33397538,		
46,	917152,	gp|M82917|WOLFLAG_1. (HPP 563)	minor flagellin flaB precursor-H.pylori,
47,	34172639,		
48,	30730068,	sp|P33024|.	similar to E.coli hypothetical nucleoside transport prot
49,	23631292,		
50,	3962777,	sp|P31122|YDEA_ECOLI.	similiar to CHLORAMPHENICOL RESISTANCE PROTEIN,

FIGURE 1

51.	24215,	sp|P19933|GLTS_ECOLI. (HPP 227)	sodium/glutamate symport carrier protein.
52.	3964593,		
53.	3991067,		
54.	24410643,		
55.	47290919,		
56.	10742963,		
57.	16422591,		
58.	23490686,		
59.	875042,	sp|P28573|NTPR_RAT. (HPP 549)	SODIUM-DEPENDENT PROLINE TRANSPORTER.
60.	4562712,	gp|U09005|VPU09005_4. (HPP 195)	channel component of the sodium-type flagellar motor.
61.	23594838,		
62.	2150290,		
63.	30471091,	sp|P08089|. (HPP 486)	encodes the serologically diverse protein M in Streptococci
64.	4821082,		
65.	23631317,	sp|P03819|KEFC_ECOLI. (HPP 113)	potassium efflux system protein.
66.	19531291,	sp|P16676|CYSA_ECOLI. (HPP 424)	SULFATE TRANSPORT ATP-BINDING.
67.	36573502,	sp|P26093|HEL_HAEIN. (HPP 540)	outer membrane protein P4 precursor.
68.	7116626,		
69.	12617677,		
70.	34495938,	sp|P33916|YEJF_ECOLI. (HPP 225)	HYPOTHETICAL ABC TRANSPORTER.
71.	24218968,		
72.	24634750,	. (HPP 226)	methyl-accepting chemotaxis protein; transmembrane receptor
73.	24132293,		
74.	20173437,	. (HPP 162)	probable cadmium-transporting ATPase.
75.	22441050,	gp|Z31376|BSFLIDST_3. (HPP 435)	flagellar protein fliS.
76.	3942217,		
77.	12520952,		
78.	31681556,		
79.	3907042,		
80.	24222885,		
81.	17497107,	. (HPP 344)	PREPROTEIN TRANSLOCASE SECA SUBUNIT.
82.	19556290,	sp|P30750|ABC_ECOLI. (HPP 19)	ATP-BINDING PROTEIN ABC.
83.	34427317,		
84.	11132778,		
85.	24645837,		
86.	35087,	sp|P13511|CZCA_ALCEU. (HPP 141)	cation efflux system membrane protein czcA.
87.	21487501,		
88.	33601578,	sp|P33913|YEJA_ECOLI. (HPP 301)	homology to HYPOTHETICAL PROTEIN IN BCR 5'REGION (FRAGMENT)
89.	26355390,	sp|P37732|MODD_AZOVI. (HPP 371)	molybdenum transport atp-binding protein.
90.	3319687,	gp|U05670|HIU05670_2. (HPP 542)	influenzae type B lipooligosaccharide.
91.	7225666,	sp|P13511|CZCA_ALCEU. (HPP 431)	cation efflux system membrane protein czcA.
92.	4826401,		
93.	867183,		
94.	21573938,	gi|495471|gp|U07145|. (HPP 147)	vacuolating cytotoxin of Hpylori.
95.	21563752,		
96.	2111040,		
97.	10037799,		
98.	23437502,		
99.	32462543,		
100.	20976500,		
101.	1038312,		
102.	14494077,	gp|Z12001|RFCRP_1. (HPP 69)	chloramphenicol resistance protein.
103.	4714375,		

FIGURE 1 CONT'D

104,	23564012,		
105,	5879160,		
106,	12694087,		
107,	22667967,	gp|U05670|HIU05670_2, (HPP 167)	influenzae type B lipooligosaccharide.
108,	14063518,	sp|P16439|FLGG_SALTY, (HPP 58)	flagellar basal-body rod proteins.
109,	23531562,	sp|P12699|ATPE_BACME, (HPP 193)	H+-transporting ATP synthase.
110,	6845425,	sp|P35100|, (HPP 536)	reacts with antibodies to chloroplast envelope proteins.
111,	22265691,	sp|P37388|XYLG_ECOLI, (HPP 153)	D-XYLOSE TRANSPORT ATP-BINDING PROTEIN.
112,	26588588,	gi|439981|gp|U04619|, (HPP 305)	flagellar hook polypeptide.
113,	14094816,		
114,	26366312,	sp|P22188|MURE_ECOLI, (HPP 302)	UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE.
115,	26423583,		
116,	23441078,	(HPP 180)	weak homology to membrane-associated c-type cytochrome.
117,	6696887,		
118,	29531590,		
119,	6848287,	sp|P31134|POTG_ECOLI, (HPP 537)	putrescine transport atp-binding.
120,	36131282,		
121,	16100038,		
122,	2548562,		
123,	1581937,		
124,	35156938,	gp|X79134|EHK18SAW_1, (HPP 402)	antigen [Entamoeba histolytica].
125,	1071890,	sp|P08006|OPPC_SALTY, (HPP 14)	oligopeptide permease membrane protein.
126,	20836042,		
127,	2082012,		
128,	6136430,		
129,	5083193,	sp|P37446|, (HPP 503)	PHOSPHOLIPASE A1.
130,	33399142,	sp|P13511|CZCA_ALCEU, (HPP 376)	cation efflux system membrane protein czcA.
131,	40339452,		
132,	917200,		
133,	4490717,		
134,	22140787,		
135,	2855006,		
136,	10664078,		
137,	24416083,		
138,	1411681,		
139,	1181418,		
140,	24407533,		
141,	24089437,	sp|P23894|, (HPP 265)	HEAT SHOCK PROTEIN HTPX PRECURSOR.
142,	24651083,	sp|P35620|FLHA_BACSU, (HPP 90)	flagellar biosynthesis protein flhA.
143,	16219090,		
144,	14572133,		
145,	5325005,		
146,	34574062,	gp|M13463|ECOCHE3, (HPP 221)	chemotaxis protein cheY.
147,	24070250,		
148,	23439633,		
149,	26614041,	gp|U07145|HPU07145_2, (HPP 306)	vacuolating cytotoxin - Helicobacter pylori.
150,	24798427,		
151,	24806290,		
152,	9776562,		
153,	32140663,		
154,	34194093,		
155,	4339708,		
156,	36134661,		

FIGURE 1 CONT'D

157,	3261306,		
158,	16225006,	sp|P28635|YAEC_ECOLI, (HPP 91)	Outer membrane 30K protein,
159,	33595708,		
160,	17787558,	sp|P30858|ARTP_ECOLI, (HPP 108)	ARGININE TRANSPORT ATP-BINDING PROTEIN
161,	24396937,		
162,	35360843,		
163,	32609403,	gp|U05676|HPU05676_2, (HPP 347)	vacuolating cytotoxin,
164,	32705252,	sp|P10740|, (HPP 368)	PHOSPHATIDYLSERINE DECARBOXYLASE,
165,	429192,		
166,	22692187,	sp|P33979|, (HPP 170)	FLAGELLAR P-RING PROTEIN PRECURSOR.
167,	10009666,	sp|Q03203|, (HPP 11)	INTEGRAL MEMBRANE PROTEIN.
168,	19536458,	sp|P37169|MVIN_SALTY, (HPP 15)	VIRULENCE FACTOR MVIN.
169,	5194840,		
170,	3906963,		
171,	23486342,	sp|P14900|MURD_ECOLI, (HPP 196)	UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATELIGASE.
172,	19536375,		
173,	17089217,		
174,	23635968,	sp|P13511|CZCA_ALCEU, (HPP 204)	cation efflux system proteins,
175,	25992137,	sp|Q02114|CWLB_BACSU, (HPP 289)	N-ACETYLMURAMOYL-L-ALANINE AMIDASE CELL WALL HYDROLASE AUTOLYSIN.
176,	14455461,		
177,	45914063,		
178,	16984442,	sp|P35528|FLIP_BACSU, (HPP 104)	flagellar biosynthetic protein fliP.
179,	12120938,		
180,	23439055,		
181,	32636635,		
182,	3933437,		
183,	24328910,		
184,	29479681,	sp|P13036|FECA_ECOLI, (HPP 322)	IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR.
185,	4177212,		
186,	26351567,		
187,	20415937,		
188,	24003758,	sp|P21458|SP3E_BACSU, (HPP 218)	spoIIIE gene product,
189,	23853165,	(HPP 209)	iron(II) transport system,
190,	26052137,		
191,	23468781,	. (HPP 153)	penicillin-binding protein 2,
192,	14726542,		
193,	6523427,		
194,	13704718,		
195,	2340814,		
196,	14642217,		
197,	5875152,	sp|P37734|MODB_AZOVI, (HPP 315)	molybdate-binding periplasmic protein precursor,
198,	104792,	sp|P15932|FLGK_SALTY, (HPP 5)	FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1,
199,	34265691,	sp|Q03523|MURE_BACSU, (HPP 343)	UDP-N-ACETYLMURAMYL-TRIPEPTIDE SYNTHETASE,
200,	5440436,	sp|P07176|PAL_ECOLI, (HPP 512)	peptidoglycan-associated lipoprotein,
201,	24078837,	sp|P23452|, (HPP 222)	component of flagellum,
202,	12343763,		
203,	19626250,	pir|S|S09411, (HPP 121)	spoIIIE gene product,
204,	4728193,		
205,	1416312,		
206,	31413433,	. (HPP 344)	dGTP triphosphohydrolase and periplasmic protease gene,
207,	26758437,		
208,	10553192,		
209,	14480927,		

FIGURE 1 CONT'D

210,	12897656,		
211,	260941,		
212,	3242337,	sp|P31438|YICM_ECOLI,	
213,	21486677,	. (HPP 140)	penicillin-binding protein 5.
214,	6933202,		
215,	11924177,		
216,	3166040,		
217,	3360130,		
218,	2915903,		
219,	203192,	sp|Q01960|FLHF_BACSU, (HPP 128)	flagellar biosynthesis protein flhF,
220,	36203402,	sp|P02913|, (HPP 420)	integeral membrane protein,
221,	26261040,	gp|U13166|RMU13166_3, (HPP 247)	chemotaxis protein cheY,
222,	23492181,	sp|P33650|FEOB_ECOLI, (HPP 183)	iron(II) transport system,
223,	14570443,		
224,	22453166,		
225,	34573431,		
226,	10407625,		
227,	35442513,		
228,	24256572,		
229,	26301059,		
230,	13723593,		
231,	23945317,		
232,	25995917,		
233,	26197187,	gp|M31827|BACDDSA_2, (HPP 295)	cell division and sporulation protein,
234,	22164962,		
235,	32627125,		
236,	16412593,		
237,	32453958,		
238,	16459375,	gp|X70039|HPCAI_1, (HPP 100)	cytotoxicity associated immunodominant antigen (H. pylori),
239,	3906712,	sp|Q05605|EXBB_PSEPU, (HPP 427)	biopolymer transport exbD protein,
240,	32595137,		
241,	16440842,		
242,	31250333,	gi|531265|gp|D21131|, (HPP 342)	sequence predicts membrane bound protein,
243,	4708337,		
244,	11253,	sp|P17952|, (HPP 20)	N-ACETYLMURAMATE--ALANINE LIGASE,
245,	26306340,		
246,	1367157,		
247,	35704718,		
248,	423131,		
249,	186752,	sp|P19933|GLTS_ECOLI, (HPP 110)	sodium/glutamate symport carrier protein,
250,	24230058,		
251,	24238762,	sp|P17448|KGTP_ECOLI, (HPP 233)	alpha-ketoglutarate permease,
252,	24276587,		
253,	29557266,		
254,	43490713,	. (HPP 457)	glycerolphosphate auxotrophy in plsB background,
255,	16251627,		
256,	23915877,		
257,	4960952,	sp|P13036|FECA_ECOLI, (HPP 499)	iron dicitrate transport protein,
258,	25925,		
259,	23880087,		
260,	6093906,		
261,	29302003,		
262,	13726562,	sp|P33941|YOJI_ECOLI, (HPP 54)	HYPOTHETICAL ABC TRANSPORTER,

FIGURE 1 CONT'D

263,	5891412,	sp|P23282|, (HPP 318)	3-deoxy-D-manno-octulosonic acid transferase,
264,	29386577,		
265,	3906937,		
266,	2458267,	gi|495471|gp|U07145|, (HPP 261)	vacuolating cytotoxin of Hpylori,
267,	24824087,	sp|P13738|NHAA_ECOLI, (HPP 275)	NA+/H+ ANTIPORTER (E.coli),
268,	33218912,		
269,	34666680,	gp|L36317|YSCCCC2A_1, (HPP401)	Cu++-transporting P-type ATPase,
270,	783432,		
271,	24609431,		
272,	6495137,		
273,	4035783,		
274,	35417942,		
275,	24414687,		
276,	259665,		
277,	23867207,		
278,	34109763,		
279,	487750,		
280,	24411011,		
281,	4721061,	sp|P36175|GCP_PASHA, (HPP 477)	O-SYALOGLYCOPROTEIN ENDOPEPTIDASE-lacks signal sequence,
282,	5440436,	sp|P10324|PAL_HAEIN, (HPP 512)	OUTER MEMBRANE PROTEIN P6 PRECURSOR
283,	24329712,	sp|P14788|, (HPP 234)	SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA,
284,	10181942,		
285,	24036302,		
286,	677088,		
287,	5111308,		
288,	29458178,		
289,	10677187,		
290,	422937,		
291,	21511555,		
292,	1370202,		
293,	36335436,		
294,	1962590,		
295,	21976637,		
296,	24427340,	sp|P10121|FTSY_ECOLI, (HPP 254)	CELL DIVISION PROTEIN -- FUNCTIONAL HOMOLOG OF SRP RECEPTOR,
297,	114505,		
298,	35428912,	sp|P10089|HLY2_ECOLI, (HPP 410)	HAEMOLYSIN SECRETION ATP-BINDING PROTEIN,
299,	19557055,	sp|P15928|FLIF_SALTY, (HPP 114)	FLAGELLAR M-RING PROTEIN,
300,	6517040,		
301,	35837767,		
302,	289711,	sp|P19933|GLTS_ECOLI, (HPP 314)	sodium/glutamate symport carrier protein,
303,	21720017,		
304,	1256885,		
305,	25422192,		
306,	719606,		
307,	272058,		
308,	23912707,	gp|U07173|VCU07173_1, (HPP 213)	ToxR-activated (tagE) gene (Vibrio cholerae) (inner membrane),
309,	24611590,		
310,	179677,	sp|P30848|PROP_ECOLI, (HPP 109)	proline/betaine transport protein,
311,	5083577,		
312,	22682813,		
313,	2843912,		
314,	24039587,		
315,	907827,		

FIGURE 1 CONT'D

316.	2035936.	gp|U05676|HPU05676_2.	(HPP 1264) vacuolating cytotoxin Hpylori.
317.	978477.	gp|L28919|STRFBPSA_1.	(HPP 3653) fibrinogen-binding protein FBP54 may be a surface antigen) 7
318.	10737627.		
319.	3953143.		
320.	197166.	sp|P08776|K2C8_XENLA.	(HPP 3577) KERATIN- TYPE II CYTOSKELETAL-intermediate filament.
321.	33476715.	sp|P16680|PHNA_ECOLI.	(HPP 3644) alkylphosphonate uptake genes A through O.
322.	14313885.	gp|L26016|DVUDCRG_1.	(HPP 3456) aspartate chemoreceptor.
323.	34489549.	gi|309688|gp|L04161|.	(HPP 4358) Plasmodium falciparum gametocyte specific antigen.
324.	3958537.		
325.	1204418.	sp|P15035|.	(HPP 3569) ROD SHAPE-DETERMINING PROTEIN.
326.	9267037.		
327.	21742157.		
328.	14257751.	sp|P15876|MRAY_ECOLI.	(HPP 2574) PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE.
329.	25605166.		
330.	23958179.		
331.	4882763.	sp|P03819|.	(HPP 1123) GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN.
332.	19531291.	sp|P37388|XYLG_ECOLI.	(HPP 4354) D-xylose transport atp-binding protein xylg.
333.	4455467.		
334.	12969218.		
335.	10312562.		
336.	23475342.		
337.	35397265.		
338.	662933.		
339.	14864452.	sp|P03819|.	(HPP1453) GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN.
340.	42683.		
341.	24417212.		
342.	24488537.	sp|P08089|.	(HPP 2551) ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M.
343.	24492192.		
344.	41552656.	sp|P35640|INVA_BARBA.	(HPP2345) invasion protein A.
345.	3157067.		
346.	12400007.		
347.	21687842.		
348.	34097707.		(HPP 3258) glycerolphosphate auxotrophy in plsB background.
349.	30078126.		(HPP 3516) MEMBRANE-ASSOCIATED HYPOTHETICAL 21.7 KD.
350.	33985087.		
351.	5993958.		
352.	24395801.		
353.	1364378.	sp|P18399|FIXS_RHIME.	(HPP 27) homology to NITROGEN FIXATION; TRANSMEMBRANE (Rhizo. meliloti).
354.	11876471.	gp|U06471|RNU06471_5.	(HPP 523) lipopolysaccharide epitope.
355.	625277.		
356.	16131887.	sp|P16665|.	(HPP -13) variable antigen from Treponema.
357.	14640637.		
358.	22704567.		
359.	29298130.	sp|P16439|FLAG_SALTY.	(HPP 3317) FLAGELLAR BASAL-BODY ROD PROTEIN.
360.	24441412.	sp|P17952|.	(HPP 255) N-ACETYLMURAMATE--ALANINE LIGASE.
361.	14662202.	sp|P35652|HRPN_BURSO.	(HPP 74) HYPERSENSITIVITY RESPONSE SECRETION PROTEIN.
362.	80257.		
363.	30703183.		
364.	26054702.	sp|P15929|FLGH_SALTY.	(HPP2472) flagellar basal body L-rin; protein.
365.	4787562.		
366.	23598962.		
367.	234391.		
368.	34179577.		

FIGURE 1 CONT'D

369,	34253912,	
370,	24882763,	sp|P33134|FLIQ_ECOLI, (HPP 270) flagellar biosynthetic protein fliQ,
371,	50062,	
372,	1218751,	
373,	4687507,	
374,	23494043,	
375,	23442642,	
376,	38080063,	
377,	4572168,	
378,	6281956,	
379,	23437741,	
380,	25478375,	sp|Q03475|LAFB_VIBPA, (HPP 279) flagellar distal capping protein homolog,
381,	10580417,	gp|U09868|ECU09868_9, (HPP 10) INVOLVED IN F PILUS ASSEMBLY,
382,	4035262,	
383,	34099062,	
384,	85786,	
385,	17086587,	sp|P08150|PBP2_ECOLI, (HPP 105) D-alanyl-D-alanine carboxypeptidase,
386,	22542803,	
387,	10723412,	sp|P33916|YEJF_ECOLI, (HPP 15) hypothetical abc transporter in bcr 5'region,
388,	11719687,	
389,	32236462,	
390,	14574201,	
391,	40409281	
392,	16281449,	sp|P37105|SRP4_BACSU, (HPP 93) signal recognition particle protein,
393,	36523442,	
394,	882827,	
395,	2774062,	
396,	36111066,	
397,	31262,	
398,	630,	
399,	392900,	sp|P15921|, (HPP 426) 190kD surface antigen,
400,	23646885,	
401,	13178562,	
402,	4895327,	gp|X72832|SEDEXB_5, (HPP 446) stringent response-like protein,
403,	21503772,	
404,	2001403,	sp|P35162|YX16_BACSU, (HPP 124) hypothetical protein X,
405,	5878208,	
406,	22303918,	
407,	4698838,	sp|P02918|, (HPP 474) penicillin binding protein,
408,	2445812,	
409,	22370182,	, (HPP 160) H.influenzae lic-1 operon licA-licD genes,
410,	16406581,	sp|P27841|CORA_ECOLI, (HPP 96) MAGNESIUM AND COBALT TRANSPORT PROTEIN,
411,	20023400,	
412,	30603402,	
413,	4095342,	
414,	23728388,	sp|P31652|NTS1_RAT, (HPP 207) serotonin transport protein,
415,	24406401,	
416,	3385833,	
417,	14344378,	
418,	32600912,	
419,	30283516,	
420,	25625192,	
421,	30081291,	

FIGURE 1 CONT'D

422,	5078593,		
423,	23446896,		
424,	19537968,		
425,	32663212,		
426,	34189716,		
427,	24609593,	sp|P23878|FEPC_ECOLI,	(HPP 263) ferric enterobactin transport protein fepC.
428,	9954743,	gi|471729|gp|U05676|,	(HPP 538) weak similarity to vacA (duplication?).
429,	1408,		
430,	3930468,		
431,	84691,	sp|P37169|MVIN_SALTY,	(HPP 57) VIRULENCE FACTOR MVIN.
432,	13865928,		
433,	32036662,		
434,	3953952,		
435,	291700,	gi|471729|gp|U05676|,	(HPP 316) weak vacA similarity.
436,	24708129,	,	penicillin-binding protein 2,
437,	30100332,	sp|P23847|DPPA_ECOLI,	(HPP 332) PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR,
438,	4492217,		
439,	10745275,		
440,	31262,		
441,	289077,		
442,	24818802,		
443,	10353192,	sp|Q05605|EXBB_PSEPU,	(HPP 5) biopolymer transport exbB protein.
444,	24104558,	pir|S|B4AG58,	(HPP 225) VirB4 homolog,
445,	3203142,	sp|P07893|ATSY_SYNP6,	(HPP 349) PROBABLE COPPER-TRANSPORTING ATPASE,
446,	32144532,		
447,	4740887,		
448,	4548792,		
449,	34658285,	sp|P33231|LCTP_ECOLI,	(HPP 400) L-LACTATE PERMEASE,
450,	4766691,		
451,	36520792,	gi|459690|gp|L29189|,	(HPP 422) methyl-accepting chemotaxis protein,
452,	4744128,		
453,	29454837,	sp|P16439|FLGG_SALT,	(HPP 320) flagellar basal-body rod proteins
454,	15039062,		
455,	4805318,		
456,	36594167,		
457,	785437,		
458,	23526667,		
459,	156587,	sp|P07365|CHEW_ECOLI,	(HPP 84) chemotaxis protein cheW,
460,	15824052,	gi|459688|gp|L29189|,	(HPP 57) transmembrane receptor,
461,	4578469,		
462,	29844512,		
463,	24415917,		
464,	24298127,	gp|L23426|NGOPHOSPHO_1,	(HPP 236) phosphoglucomutase,
465,	32952,	sp|P31220|YHBG_ECOLI,	(HPP 364) PROBABLE ABC TRANSPORTER,
466,	32422343,		
467,	23493756,		
468,	214812,	sp|P33231|LCTP_ECOLI,	(HPP 139) L-lactate permease,
469,	1179838,		
470,	98191,		
471,	14714687,	sp|Q08382|MODB_RHOCA,	(HPP 79) molybdenum transport system permease,
472,	3317501,	gi|495471|gp|U07145|,	(HPP 370) vacuolating cytotoxin of Hpylori,
473,	19541302,		
474,	23438840,		

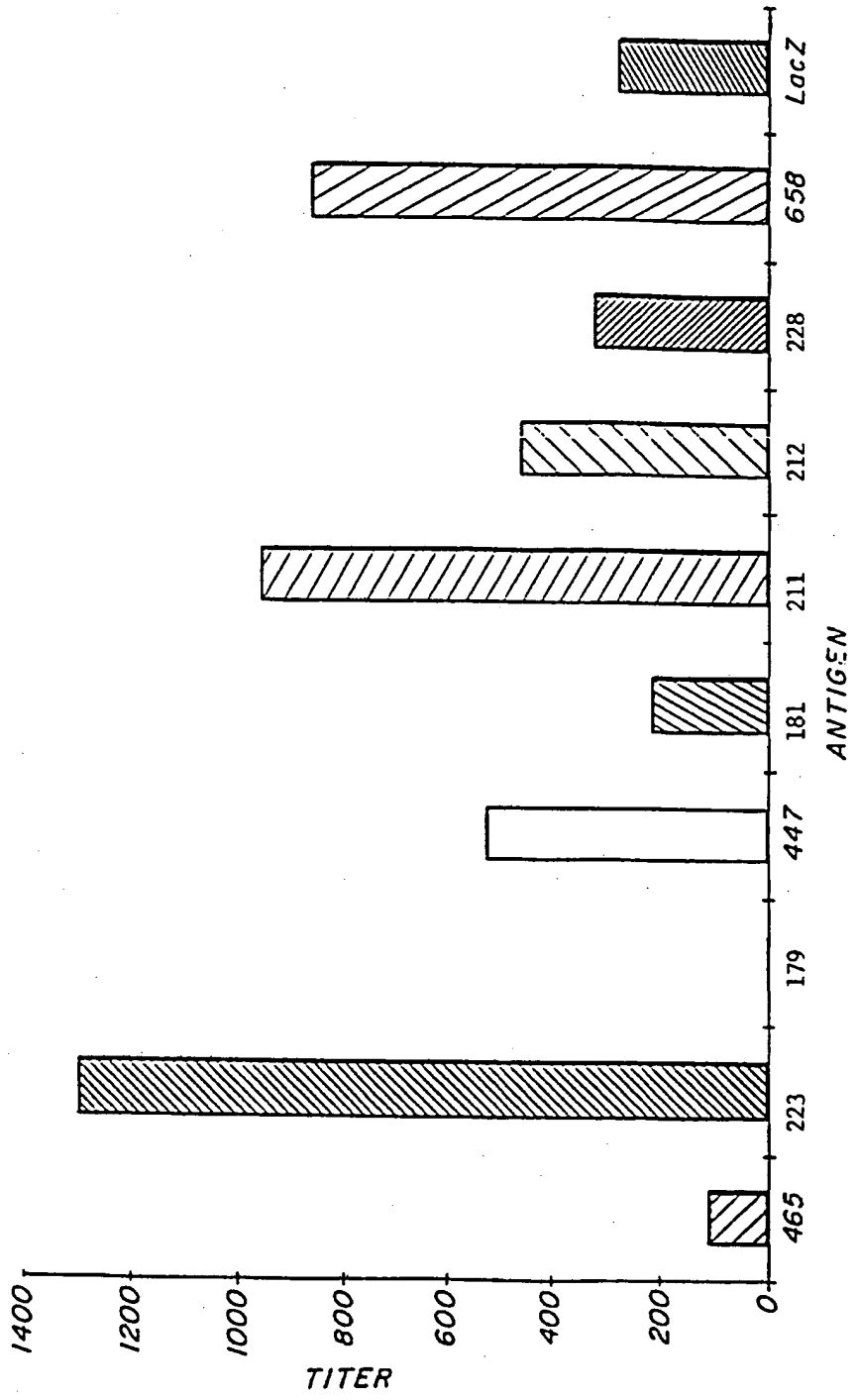
FIGURE 1 CONT'D

475,	2738378,	
476,	22460468,	gp|X76422|NSPENA2_1. (HPP 165) penicillin-binding protein 2,
477,	26380318,	sp|P15933|FLIC_SALTY. (HPP 303) FLAGELLAR MOTOR SWITCH PROTEIN F,
478,	24803280,	
479,	29843937,	gi|495471|gp|U07145|. (HPP 320) vacuolating cytotoxin of Hpylori,
480,	1431462,	gp|L16627|PASPLP123A_2. (HPP 65) outer membrane 30.2K protein,
481,	34089087,	
482,	35445843,	
483,	22687687,	
484,	23473437,	
485,	23515833,	
486,	30662792,	sp|P10408|SECA_ECOLI. (HPP 337) PREPROTEIN TRANSLOCASE SECA SUBUNIT,
487,	1171928,	sp|P35538|FLHB_BACSU . (HPP 23) FLAGELLAR BIOSYNTHETIC PROTEIN FLHB,
488,	21767890,	
489,	4882652,	
490,	23539006,	
491,	6517192,	sp|P37105|SRP4_BACSU. (HPP 529) signal recognition particle protein,
492,	1933,	
493,	22447252,	
494,	14645905,	gi|520402|gp|U03552|. (HPP 76) sensor protein,
495,	10675632,	sp|P23445|FLII_BACSU. (HPP 12) H+-transporting ATP synthase alpha chain homolog,
496,	23831562,	
497,	32704686,	
498,	24816915,	
499,	24219012,	
500,	4897177,	
501,	4486092,	sp|P25536|YHDE_ECOLI. (HPP 460) E.coli mreD gene Rod shape-determining protein ,
502,	21618785,	sp|P05353|VIB4_AGRT9. (HPP 148) VIRB4 PROTEIN PRECURSOR,
503,	16603418,	
504,	4551291,	
505,	23867687,	
506,	25976418,	
507,	25525277,	(HPP 282) flagellar motor switch protein fliM,
508,	32431687,	
509,	4531568,	
510,	19720300,	
511,	24413512,	
512,	4570262,	
513,	29500075,	sp|P38489|NFSI_ECOLI. (HPP 323) OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE,
514,	30089217,	
515,	134666,	
516,	391313,	
517,	4726503,	
518,	26172627,	
519,	24495312,	
520,	30082267,	
521,	24300682,	
522,	25398250,	
523,	23610905,	
524,	23573294,	
525,	485375,	
526,	1206675,	
527,	23567137,	gp|U07145|HPU07145_2, HPP 197 vacuolating cytotoxin - Helicobacter pylori,

FIGURE 1 CONT'D

528.	30728393.	sp|P32113|ATKA_ENTFA. (HPP 340)	POTASSIUM/COPPER-TRANSPORTING ATPASE A.
529.	1385937.		
530.	20032561.	sp|P07117|PUTP_ECOLI. (HPP 126)	SODIUM/PROLINE SYMPORTER.
531.	4414000.		
532.	34489543.	gi|415692|gp|L26015|. (HPP 345)	putative chemoreceptor.
533.	35949212.		
534.	1464715.	sp|P33231|LCTP_ECOLI. (HPP 77)	L-lactate permease.
535.	35336707.		
536.	16839562.		
537.	25501501.		
538.	23671689.		
539.	4491093.		
540.	194415.		
541.	14713512.	sp|P22565|LYTB_ECOLI. (HPP 78)	INVOLVED IN PENICILLIN TOLERANCE-has signal peptide seq.,
542.	4882318.		
543.	663530.		
544.	16305252.		
545.	16603381.		
546.	33394230.		
547.	16406265.	sp|P26601|. (HPP 95)	integral protein in inner membrane,
548.	495312.	sp|Q03523|. (HPP 495)	ACETYLMURAMOYLALANYL-D-GLUTAMATE-DIAMINOPIMELATE LIGASE.
549.	15807794.		
550.	11878127.		
551.	3242952.	gi|487637|gp|U09364|. (HPP 356)	similarity with eukaryotic myosins.
552.	7031343.		
553.	13673328.		
554.	50253.	sp|P10413|HTPG_ECOLI. (HPP 50)	heat shock protein C62.5 - chaperone-ATPase activity.
555.	13727311.	gi|155338|gp|M82917|. (HPP 55)	flagellin.
556.	5265957.	gi|160409|gp|M69183|. (HPP 508)	surface antigen.
557.	12697338.	sp|Q01465|MREB_BACSU. (HPP 41)	rod shape-determining protein envB.
558.	20911583.		
559.	21699087.		
560.	2461062.		

FIGURE 1 CONT'D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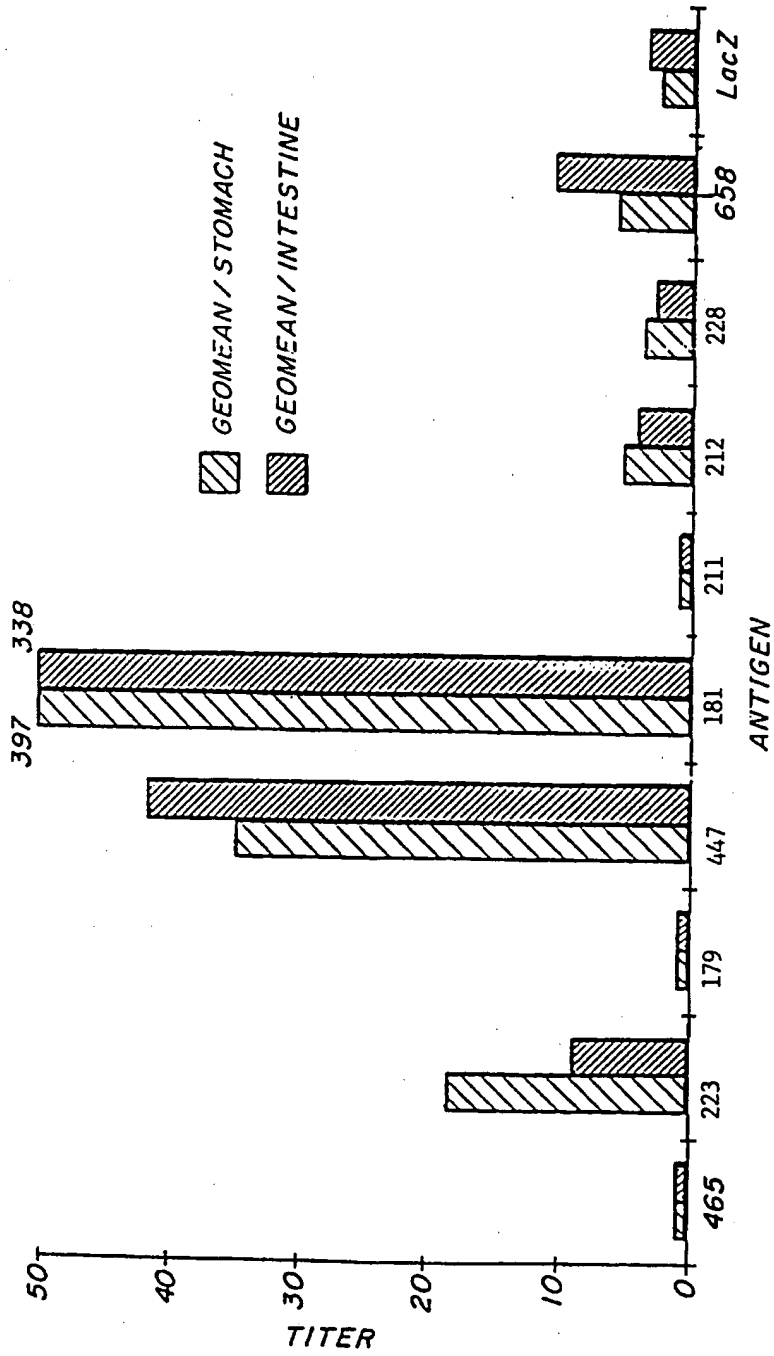
ANTIGEN

FIGURE 2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GEOMEAN / INTESTINE
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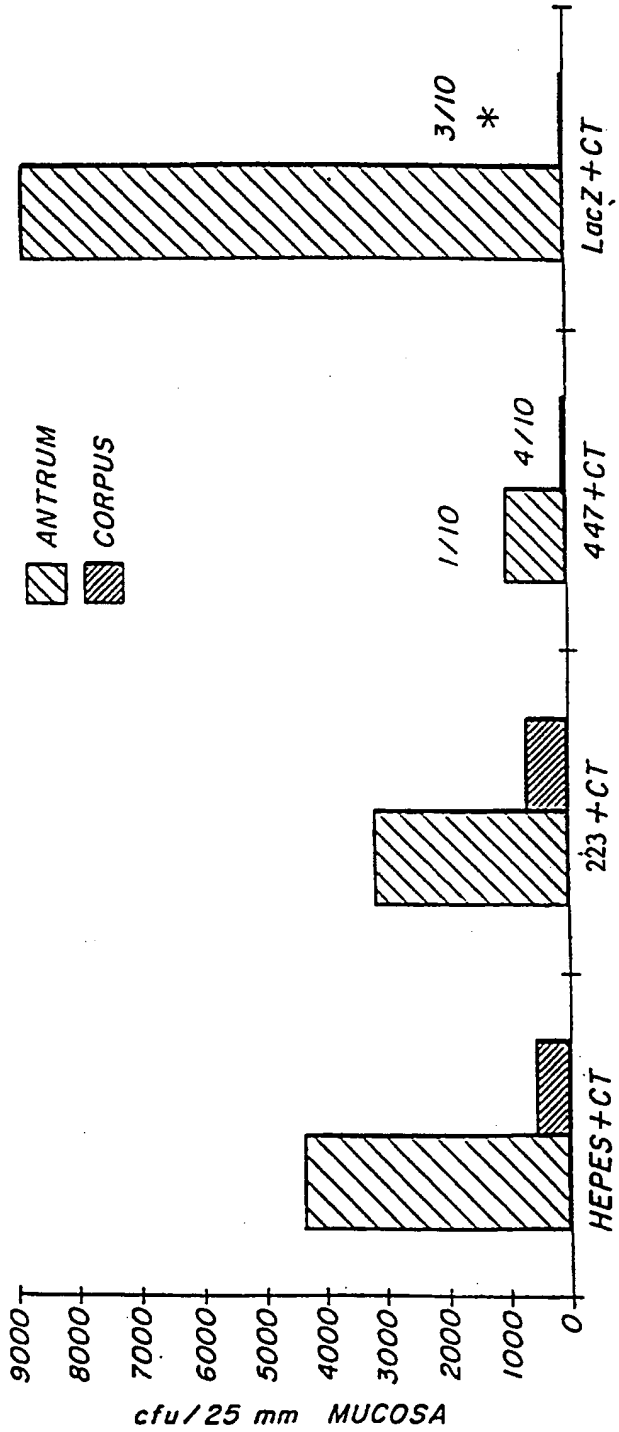
ANTIGEN

FIGURE 3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CORPUS
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cfu/25 mm MUCOSA
HEPES+CT
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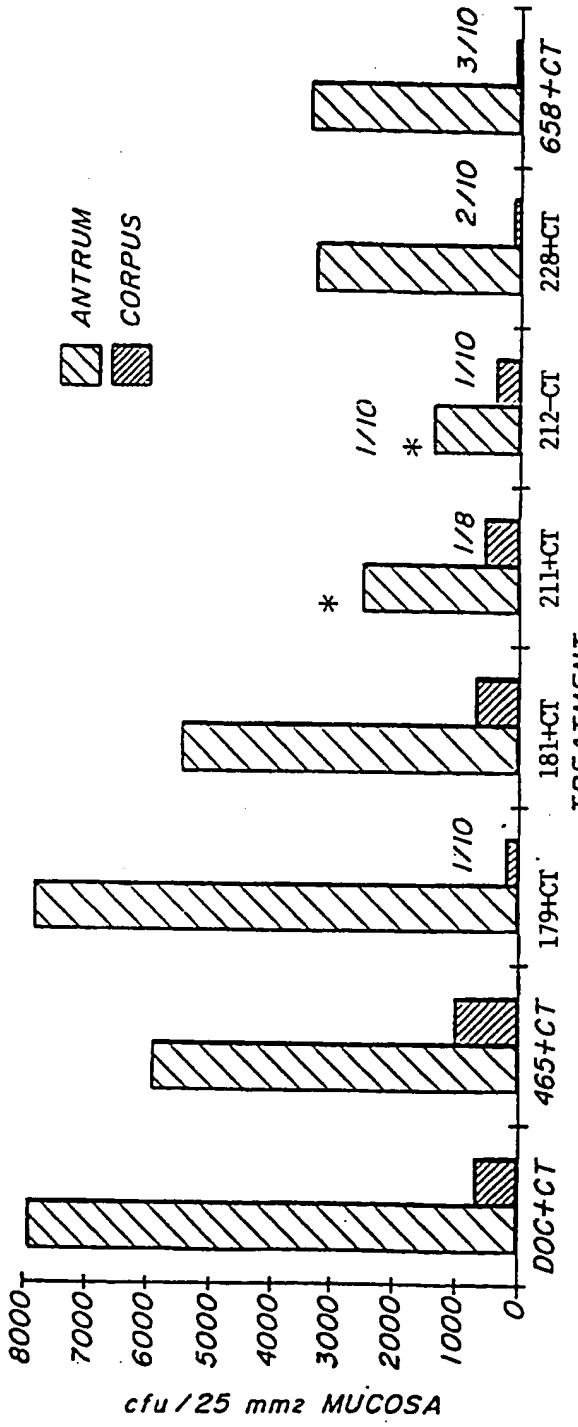
447+CT
LacZ+CT
TREATMENT

FIGURE 4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cfu / 25 mm2 MUCOSA
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1/10
181+CT
211+CT
1/8
212-CT
1/10
228+CT
2/10
658+CT
3/10
TREATMENT
*
*

FIGURE 5

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542

A. CLASSIFICATION OF SUBJECT MATTER
IPC(6) :C07H 21/04
US CL :536/23.7
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, BIOSIS, CA, DERWENT
search terms: H. pyluri, vaccine, gene, protein

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,403,924 A (COVER et al.) 04 April 1995.	1-7
A	US 5,434,253 A (THOMPSON et al.) 18 July 1995.	1-7
A, P	US 5,527,678 A (BLASER et al.) 18 June 1996.	1-7

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 13 MARCH 1997	Date of mailing of the international search report 07 APR 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer KENNETH R. HORLICK Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7 regarding SEQ ID NO: 9, 46, 59, 69, 83, 97, 98, 101, 109, and 114

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.